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## SEARCH REQUEST FORM

## Scientific and Technical Information Center

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Requester's Full Name:  An Unit:  Mail Box and Bldg/Room Location:  If more than one search is submises provide a detailed statement of the submitty of the invention. Define any terms to mown. Please attach a copy of the cover slinity of the invention.  Title of Invention:  Inventors (please provide full names):  Earliest Priority Filing Date:	itted, please prior	searches in order of secifically as possible the s ms. and registry numbers, and ms. and registry numbers, and	need. ***********************************

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(ZYMO ) ZYMOGENETICS INC.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AAB10644 AAB10651 AAB10651 AAB10651 AAB13414 AAB24412 AAY896858 AAY59285 AAB10639 AAY8955 AAB10639 AAY84557 AAB10636	AAB48653 AAY96864 AAY71130 AAB60888 AAB48663 AAB10652 AAB10643 AAB10643 AAB10643	AA. owth tivit rivit Alzh re; w
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Sheppard PO, Gilbertson DG;

Hart CE,

WPI; 2000-687541/67

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AAY96861;

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The invention relates to the human growth factor homologue zvegf4

(AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member

(A CAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member

(C of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial)

growth factor) family. Zvegf4 has a growth factor domain (AAB48654)

(C AAB48655) which has a beta barrel structure. Zvegf4 has PDGF-like

activity, having mitogenic activity on fibroblasts, vascular smooth

muscle cells and pericytes, and has also been shown to stimulate bone

activity, having mitogenic activity on fibroblasts, vascular smooth

muscle cells and pericytes, and has also been shown to stimulate bone

crowgf4 or fragments thereof, particularly human zvegf4/human zvegf4

tusions; expression constructs and host cells comprising human zvegf4 or fragments thereof, particularly human zvegf4/human zvegf4

crowff4 or fragments thereof, particularly human zvegf4, an antibody

which binds to human zvegf4 or a fragment thereof; a method of activating

a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a

call-surface PDGF receptor using a zvegf4-derived polypeptide; a

method of modulating the proliferation, differentiation or

metabolism of bone cells, comprising exposing bone cells to

zvegf4-derived polypeptides; and a method of detecting a genetic

abnormality in the zvegf4 gene of a patient. Zvegf4 proteins and derived

fragments may be used to stimulate tissue development or repair, or

callular differentiation or proliferation. They are particularly used

the treatment or repair of liver damage, and may also be used to

modulate neurite growth (e.g., in the treatment of Alzeimer's disease or

multiple sclerosis). Due to their osteogenic activity, they may also be

callular differentiation or proliferation. They are particularly

cand endothelial precursor stem cells, which may be used to

multiple sclerosis). Which may be used to be used to be na endone expansion and mobilisation of the multiple sc
                                                                                                                                                  useful
                                                                                                                                                                                                            for treating liver damage, ischemia, multiple sclerosis and
                                                                                                                                      Growth factor homologs and the nucleic acids that encode them,
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                                                                                                                                                                                                                                                                     Alzheimer's disease -
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N-PSDB; AAC81583
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.; 0 21; Length 345; 0; Indels Score 1848; DB 21; Pred. No. 2.3e-182; 0; Mismatches 0; 100.0%; Query Match 100. Best Local Similarity 100. Matches 345; Conservative

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Gaps

180 240 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300 9 9 PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL 61 121 121 181 181 241 δŏ g ò g ŏ g φ g ŏ

VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345 301 à a

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AAY96861 standard; Protein; 345 AA AAY96861 RESULT

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Gaps

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1 MLLLGLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS

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Query Match 100.0%; Score 1848; DB 21; Length 345; Best Local Similarity 100.0%; Pred. No. 2.3e-182; Matches 345; Conservative 0; Mismatches 0; Indels 0;

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This shows a murine ZVEGF3 a novel vascular endothelial growth factor homologue. Polypeptides comprising an epitope-bearing portion human or murine ZVEGF3 are claimed. The growth factors comprise a growth factor comprise a growth factor comprise a growth factor comprise a growth factor domain and a CUB domain (generic Sequence motifs are shown in AAY96859 arrangement of Cystelior residues and beta-strands that is characteristic crangement of Cystelior Extructure of the platelet-derived growth factor (PDGF) family. The CUB domain shows homology to CUB domains in neurophilns, human bone morphogenetic protein.) porcine seminal plasma protein, bovine acidic seminal fluid protein and Xenopus laevis tolloid-like protein. Structural analysis and homology predict that zvegf3 polypeptides complex with a second polypeptide to form multimeric zvegf3 is useful for stimulating the growth of fibroblasts or smooth muscles cells, for activating cell surface PDGF alpha receptor and for inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is useful for stimulating the growth, regeneration and maintenance, as well as tissue maintenance and repair processes. ZVEGF3 diabetic retinopathy, isohemic limb disease, peripheral vascular characterial parameters are useful for treating concer, rheumatoid arthritis, disbeming land disease, peripheral vascular intimal physophala.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel gregf3 polypeptides and nucleotides encoding them useful for stimulating growth of smooth muscle cells and fibroblasts comprising an epitope bearing portion of a specific amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atherosclerosis, wound healing, chronic liver disease and haemangioma formation. ZVEGF3 can also be used to modulate neurite growth and development of the nervous system, and for treating neurodegenerative
                                                                                                                     Vascular endothelial growth factor; homologue; zvegf3; CUB domain; Cysteine Knot; platelet-derived growth factor; pDGF; neuropilin; chromosome 4q28.3; cytostatic; anti-psoriatic; anti-inflammatory; anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shoemaker KE;
                                                                              Murine vascular endothelial growth factor homologue, ZVEGF3.
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Gilbertson DG, West JW;
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N-PSDB; AAA51527.
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the PDGF-C
                                                                                                                                                                                                                                                                                                           growth factor; heparin; connective tissue; wound healing; VEGF-F; fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth; choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents murine platelet-derived growth factor (PDGF-C) (formally designated VEGF-F). PDGF-C polypeptides have the ability to stimulate and enhance proliferation or differentiation,
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mll1g1111tsalagqrtgtraesnlssklg1ssdkegngvgdprhervvtisgngsihs
                                                            GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS
                                                                     LKEEVKLYSCTPRNFSVSIREELKRTDT1FWPGCLLVKRCGGNCACCLHNCNECQCVPRK
                          PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL
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                                                                                                                                                                                                                                                                                                    Platelet-derived growth factor C; PDGF-C; cell proliferation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel DNA encoding PDGF-C useful to stimulate or enhance differentiation, growth and motility of cells expressing
                                                                                                                                                                             301 VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
                                                                                                                                                                                                                                                                                                                                     carcinoma; erythroleukemia; tissue remodelling
                                                                                                                                                                                                                                                                                    A murine platelet-derived growth factor C (PDGF-C).
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Betsholz C;
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03-DEC-1998;
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and/or growth or motility of cells expressing a PDGF-C receptor. PDGF-C polypeptides can be used in pharmaceuticals for promoting cell proliferation, preferably in combination with one other growth factor and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also be used for stimulating connective tissue or wound healing. The PDGF-C polypeptide can be enzymatically processed to generate the active truncated form of PDGF-C and used to regulate the receptor-binding specificity of PDGF-C and used to regulate the receptor-binding mitogenesis in a mammal and to induce PDGF alpha receptor activation. PDGF-C antagonists can be used to inhibit tumour growth of a tumour expressing PDGF-C in a mammal. Specific types of human tumours, e.g. choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEGF-E; human; vascular endothelial cell growth factor; wound repair; treatment; cardiovascular disorder; endothelial disorder; therapy; tissue generation; regeneration; cardiac hypertrophy; cancer; detection; angiogenic disorder; age-related macular degeneration; vascular disease; neovascularization; tumor; gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of
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                                                                                                                                                                                                                                                                                                                                                                                                        and erythroleukemia, can be identified by testing for expression of PDGF-C. PDGF-C antagonists can also be used to inhibit tissue remodelling during invasion of tumour cells into a normal population cells. Antagonists can also be used to treat fibrotic conditions,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKFFHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 345;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1848; DB 21; 100.0%; Pred. No. 2.3e-182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                especially found in the lung, kidney or liver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345 AA;
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tranquillizer, vulnery and cardiant activity. VEGF-E can be administered therapeutically, especially by expressing encoding polynucleotides, to therapeutically, especially by expressing encoding polynucleotides, to tranquillizer, vulnery and cardiant activity. VEGF-E can be administered that cardiavascular or endothelial disorders in mammals, especially humans. It is useful in wound repair and tissue generation and regeneration, and may especially be used to treat cardiac hypertrophy or regeneration, and may especially be used to treat cardiac hypertrophy or can be administered to treat disorders as above. VEGF-E can be used to soreen for antagonists and agonists, and the antagonists administered to treat anjoigenic disorders in mammals (especially humans) e.g. cancer or age-related macular degeneration. It can be used to generate antibodies, useful therapeutically as antagonists, as above. The antibodies are also cardiovascular, endothelial or angiogenic disorders in mammals (e.g. vascular disease, or neovascularization associated with tumor formation of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding the antibody with a tissue sample and detecting formation of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding the mammals, by detecting abnormally high or low VEGF-E gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences or for gene mapping. This sequence represents the human VEGF-E protein described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                         New growth factor polypeptide useful for treating cardiovascular or endothelial disorders, e.g. cardiac hypertrophy
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87.0%; Pred. No. 1.2e-163;
Live 27; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 2; 122pp; English
98US-0040220.
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Matches 300; Conservative
                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                   WPI; 1999-580306/49.
                                                                                                                                                                                            Ferrara N, Kuo SS;
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17-MAR-1998;
02-NOV-1998;
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VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345

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Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein.
      AAY41766 standard; Protein; 345 AA.
                                                  Human PRO200 protein sequence.
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98US-0079689
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98US-0079786
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98US-0082568
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98US-0083392
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                                   (first entry)
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                                   07-DEC-1999
                                                                                             Homo sapiens
                                                                                                           W09946281-A2
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15-APR-1998;
15-APR-1998;
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17-MAR-1998
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20-MAR-1998,
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29-APR-1998;
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                     AAY41766;
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AAY41766
ID AAY4
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LKEEVKLYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vascular endothelial growth factor related protein; VEGF-R protein; tissue growth inhibition; tumour growth; cancer; tissue growth; angiogenesis; coronary artery blockage.
                                                                                                                                                                                                         MLLCGLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS
                                                                   PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEFPSDGSVL
                                                                                                                                 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS
                                                                                                                                                                                           181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
                                   1 mslfglllltsalaggrqgtqaesnlsskfqfssnkeqngvqdpqheriitvstngsihs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A vascular endothelial growth factor related protein and related polynucleotide, useful for identifying antagonists and binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human vascular endothelial growth factor related protein.
                                                                                                                                                                                                                                                                                                                                    VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
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98US-0072635.
98US-0088089.
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05-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coaqulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AA233891 to AA234338, and AAY41685 to AA441774 represent polynucleotide and polypeptide sequence given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           secreted and transmembrane polypeptides and their polynucleotides,
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87.0%; Pred. No. 1.2e-163;
iive 27; Mismatches 18;
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ive 27; Mismatches 18;
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                                                                                                                                                                                                                                                                                            Conservative
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                                                                                        345 AA;
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                                                                                        Sequence
                                                                                                                                                                                                             Query Match
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Matches 30
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C (AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member of the PDGF (platelet-derived growth factor) WEGF (vascular endothelial crave) that factor) family. Zvegf4 has a growth factor domain (AAB48654) conversely and provided growth factor) was and a CUB domain (AAB48655) which has a beta barrel structure, and a CUB domain (C characterised by a PDGF cystine knot structure. Zvegf4 has PDGF-like activity, having mitogenic activity on fibroblasts, vascular smooth muscle cells and pericytes, and has also been shown to stimulate bone growth. The invention also relates to fusion proteins comprising human cycgf4 or fragments thereof, particularly human zvegf4/human zvegf4 or fragments thereof, particularly human zvegf4/human zvegf4 or custos; expression constructs and host cells comprising human zvegf4 or a fragment thereof; a method of activating which binds to human zvegf4 or a fragment thereof; a method of activating concernation of modulating the proliferation, differentiation or metabolism of bone cells, comprising exposing bone cells to comprising exposing bone cells to a zvegf4 derived polypeptides; and a method of detecting a genetic abnormality in the zvegf4 gene of a patient. Svegf4 proteins and derived fragments may be used to stimulate tissue development or repair, or cellular differentiation or proliferation. They are particularly used for the treatment of peptidoses; and modulate neurite growth (e.g., in the treatment of paralogoment of haematonic stand controlled is a controlled to the paralogoment of haematonic of haematonic of haematonic of haematonic stand colls of the paralogoment of haematonic of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used to enhance expansion and mobilisation of haematopoietic stem cells and endothelial precursor stem cells, which may be useful in the treatment of ischaemia, in wound healing, and in the modulation of the immune system. The present sequence represents human zvegf3.
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87.0%; Pred. No. 1.2e-163;
ive 27; Mismatches 18;
invention relates to the human growth factor
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Best Local Simi
Matches 300;
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AAB44322 standard; Protein; 345 AA.
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                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method for enhancing tissue growth, promoting wound healing or stimulating smooth muscle growth by administering a platelet-derived growth factor (PDGF) related protein, designated LPB or its analogue. Also described is a method of slowing the progress of atherosclerosis or treating atherosclerosis comprising the administration of an LPB antagonist. The method is useful for enhancing tissue growth, promoting wound healing and stimulating smooth muscle growth. Antagonists of LDB are useful for treating atherosclerosis. The present sequence represents human LPB, which is
                                                                                                                                                                                                                                                                                                     Enhancing tissue growth and promoting wound healing by administering platelet-derived growth factor related protein, LP8 or its analog and treating atherosclerosis by administering LP8 antagonist
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                         vascular endothelial growth factor h; tissue regeneration; vatherosclerosis; PDGF-related protein; antiarteriosclerotic.
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87.0%; Pred. No. 1.2e-163;
Live 27; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 63-64; 64pp; English
                                                                                                                                                                             99US-0127913
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Best Local Similarity
Matches 300; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 also called VEGFh.
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                                                                                           WO200059940-A2.
                                                                   Homo sapiens.
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                                                                                                                        12-OCT-2000
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sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, eg. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel PRO polypeptides and polynucleotides used in detection methods, to target bioactive molecules to specific cells, and to modulate cellular activities -
                                                                                                                                              protein; transmembrane protein; PRO; EST; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gerritsen ME;
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                                                                                              Human PRO200 (UNQ174) protein sequence SEQ ID NO:488
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87.0%; Pred. No. 1.2e-163;
iive 27; Mismatches 18;
                                                                                                                                                                 expressed sequence tag; detection; cancer
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99US-0134287.
99US-0141037.
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99WO-US28565.
99WO-US30095.
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99US-0126773.
99US-0130232.
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                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 90.2
Best Local Similarity 87.0
Matches 300; Conservative
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N-PSDB; AAC78582.
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                                                                                                                                                                                                                                                                WO200053756-A2.
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                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                               18-FEB-2000;
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06-JAN-2000;
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30-DEC-1999;
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                                               08-FEB-2001
                                                                                                                                                                                                                                                                                                                14-SEP-2000
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02-DEC-1999
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16-DEC-1999;
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AAB44322;
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AAB44322 RESULT

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VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; antiologenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynuclectide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization
                                                                                                       GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFC1HYSIIMPQVTETTSPSVLPPSS 180
                                                                                                                                                                        121 grwcgsgtvpgkqiskgnqirirfvsdeyfpsepgfcihynivmpqfteavspsvlppsa 180
                                                                                                                                                                                                                                                                       PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL
                                                                                                                                                                                                                                                         LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK
                                                                                                                                                                                                    LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
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                                                                                                                                                                                                                                                                                                             VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
                                                                                                                                                                                                                                                                                                                           Dijkmans JJH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.
                                                                                                                                                                                                                                                                                                                                                                                                      AAB10633 standard; Protein; 345 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 6; 127pp; English.
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99US-0124967.
99US-0164131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human RACE generated VEGF-X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200037641-A2.
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regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the RACE generated human VEGF-X protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VBGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300
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                                                                                                                                                                                                                                                                90.2%; Score 1667; DB 21;
87.0%; Pred. No. 1.2e-163;
ive 27; Mismatches 18;
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99US-0164131
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                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                    345 AA;
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18-MAR-1999;
08-NOV-1999;
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Matches 30
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(VEGETA) protein (IIa) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic cretinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the human VEGFTX protein cisolated from clones 4 and 7 described in the method of the invention.
                                                                                                                                                                                            New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                              invention describes a novel vascular endothelial growth factor-X
                                                                    Ä
                                                                 Gosiewska
                                                               Dijkmans JJH,
                                                               You JR,
                                                                                                                                                                                                                                                                                       English
                                                                                                                                                                                                                                                                                       Disclosure; Fig 9; 127pp;
                                                               Sprengel JJ,
                      (JANC ) JANSSEN PHARM NV
                                                                                                                            WPI; 2000-442669/38.
N-PSDB; AAA71955.
                                                                                      Xu J;
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                                                                                      Dhanaraj SN,
                                                               Gordon RD,
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ö LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL 240 240 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS 180 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300 PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEFPSDGSVL 120 9 9 Gaps 1 MLLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS ö Length 345; Indels 90.2%; Score 1667; DB 21; 87.0%; Pred. No. 1.2e-163; ive 27; Mismatches 18; Conservative Similarity 300; Query Match Best Local S Matches 241 61 61 121 181 g δ q g ò g ò δ

Q δ

301 VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345 

Ā AAB10644 standard; Protein; 345 (first entry) Human VEGF-X protein #4 19-JAN-2001 AAB10644; RESULT 12 DX DX XX

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This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has valuerary, cytostatic, antitheumatic, antiantheumatic, antiantheumatic, antiantheumatic, antiantheumatic, antiantheumatic, antiantheumatic antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues of the invention are useful for preparing medicaments for treating wounds such as dermal ulcrs, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair, proliferation of new blood vessels, tissue regeneration and organ repair, proliferation of new blood vessels, tissue regeneration. This sequence repersents a human VEGF-X protein described in the method of the invention. ; 0 vascular endothelial growth factor; human; vulnerary; cytostatic; New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; anglogeneeis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; Gaps ö Yon JR, Dijkmans JJH, Gosiewska A; Length 345; Indels sore; diabetic ulcer; burns; skin graft growth. 18; DB 21; 90.2%; Score 1667; DB 21; 87.0%; Pred. No. 1.2e-163; ive 27; Mismatches 18; Disclosure; Fig 30B; 127pp; English 98GB-0028377. 99US-0124967. 99US-0164131. Sprengel JJ, Best\_Local Similarity 87.0 Matches 300; Conservative (JANC ) JANSSEN PHARM NV WPI; 2000-442669/38 345 AA; × N-PSDB; AAA71990 WO200037641-A2 22-DEC-1998; 18-MAR-1999; 08-NOV-1999; Dhanaraj SN, Homo sapiens 21-DEC-1999; 29-JUN-2000 Gordon RD, Sequence Query Match venous δλ

GRWCGSGTVPGKQTSKGNHIRIREVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS 180 240 121 grwcgsgtvpgkqiskgnqirirfvsdeyfpsepgfcihynivmpqfteavspsvlppsa 180 PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEFSDGSVL 120 1 MLLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS LSLDLLNNAVTAFSTLEELIRYLEPDRMQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL 61 61 121 181 g g g ò δ δ

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Pred. No. 1.2e-163;

87.0%;

Best Local Similarity

300

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This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; antiologesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue regeneration and organ repair by promoting angiogenic activity c vascularization. This sequence represents the human 990126vegx protein used to illustrate the method of the invention.
                               New vascular endothelial growth factor protein, useful for treating
   241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK
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                                                                                                                                                                                                                                                                                                                                                                     AAB10650 standard; Protein; 345 AA
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08-NOV-1999;
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New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatiantirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
                                                                                                         120
                                                                                                                                    180
                                                                                                                                                             180
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                                                                              61 PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEFPSDGSVL 120
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                                        1 MLLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS
                                                                                              121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS
                                                                                                                                                                                         181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
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27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            AAB10651 standard; Protein; 345 AA.
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99US-0124967.
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300; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human VEGF-X protein #3.
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antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting anglogenic activity or vascularization. This sequence represents the human VEGF-X protein described in the method of the invention.
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                                                                                                                                                                                                             / Match 90.2%; Score 1667; DB 21;
Local Similarity 87.0%; Pred. No. 1.2e-163;
hes 300; Conservative 27; Mismatches 18;
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/note= "Asn is N-glycosylated"
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15..345
/label= Mature_Pro200
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The present sequence is that of human PRO200 or vascular endothelial growth factor E (VEGF-E), as predicted from a cDNA clone (see AAA88512) that was isolated from a glioma cell line GG1 ibrary using probes (see AAA88521-26) based on an expressed sequence tag (see AAA88522) that showed homology to VEGF. PRO200 has a predicted mol.wt. of 39,029 and a pl of about 6.06. A method for producing PRO polypeptides, including PRO200, using a host cell transformed with a vector comprising a PRO nucleic acid is claimed. The invention relates to the use of PRO polypeptides to delay, prevent or rescue retinal cells such as retinal neurons selected from photoreceptors, retinal ganglion cells, displaced retinal ganglion cells, amacrine cells, displaced amacrine cells, horizontal and bipolar neurons, and supportive cells (including Mueller cells and bigment epithelial cells) from injury, light or environmental trauma or death is caused by retinal injury, light or environmental trauma or death is caused by retinal injury, light or environmental trauma or dependantly, retinal degenerative macular degenerative described from retinitis pigmentosa, macular celars, retinopathy, retinal degenerative described in training tears, retinopathy, retinal degenerative degenerative myopia, acute retinal necrosis syndrome, traumatic chorioretinopathies or contusion such as central or branch retinal vision contusion such as central or branch retinal vision contusions and as central or branch retinal vision
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87.0%; Pred. No. 1.2e-163;
ive 27; Mismatches 18;
                        254..258
/note= "Asn is N-glycosylated"
/note= "Asn is N-glycosylated"
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S, La Fleur M,
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//note= "N-my...
127..133
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319..325
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Kuo SS,
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Kljavin IJ,
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steroid 21-monooxygenase (EC 1.14.99.10) cytochrome P450 21 - human N;Alternate names: cytochrome P450(C21B); steroid 21-hydroxylase cytochrome P450 21A2 (S;Specias: Homo sapiens (man) C;Date: O4-Dec-1986 #sequence_revision 08-Feb-1996 #text_change 03-Mar-2000 C;Accession: A25446; A00191; A27865; A32715; A21889; S26484; S29670; S29671; S26584; R;White, P.C.; New, M.I.; Dupont, B. Proc. Natl. Acad. Sci. U.S.A. 83, S111-5115, 1986 A;Title: Structure of human steroid 21-hydroxylase genes.
                                                                                                                                                                                                                                                                                                                                                                                      Cytochrome P450 21A/B mutant fusion protein - human N.Alternate names: steroid 21-monooxygenase C;Species: Homo sapiens (man) C;Date: 06-Jan-1995 #sequence_revision 17-Aug-1995 #text_change 15-Feb-1996 C;Accession: S26485; S29672 R;Helmberg, A.; Kofler, R. submitted to the EMBL Data Library, March 1991 A;Reference number: S26485
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A; Residues: 1-494 < WHI.7-
A; Cross-references: GB:Ml3936; NID:g187899; PIDN:AAA59695.1; PID:g386910
R; Higashi, Y.; Yoshioka, H.; Yamane, M.; Gotoh, O.; Fujii-Kuriyama, Y.
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100.0%; Pred. No.
ive 0; Mismatch
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C;Genetics:
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Best Local Similarity 100.
Matches 9; Conservative
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C;Keywords: fusion protein
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neurexin II-beta p
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                                    Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                               Notal number of hits satisfying chosen parameters:
                    GenCore version 4.5
Copyright (c) 1993 - 2000 Com
                                                                                                                                                                                                                                                                                                            219241 segs, 76174552 residues
                                                                                                                      5, 2001, 10:55:18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Listing first 45 summaries
                                                                                       protein search, using sw model
                                                                                                                                                                                                                                                                         Gapop 60.0 , Gapext 60.0
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O4HUC2
A26774
A26774
I54768
S104936
PB2294
T04095
S43455
A3455
A3455
G86587
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G86587
F75257
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149276
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length: 2000000000
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Query
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1: pir1:*
2: pir2:*
4: pir3:*
5: pir4:*
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Score

No. Result

0

Word size : Searched:

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Minimum DB seq Maximum DB seq

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Gaps

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Length 494; 0; Indels

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N'Alternate names: cytochrome P450(GP-1)
C;Species: Cavia porcellus (quinea pig)
C;Date: 31-Mar-1992 #sequence_revision 08-Feb-1996 #text_change 05-Mar-1999
C;Date: 31-Mar-1992 #sequence_revision 08-Feb-1996 #text_change 05-Mar-1999
C;Accession: S15135; S28205; A36154
R;Oguri, K.; Kaneko, H.; Tanimoto, Y.; Yamada, H.; Yoshimura, H.
Arch. Biochen: Biophys. 287, 105-111, 1991
A;Title: A constitutive form of guinea pig liver cytochrome P450 closely related to p
A;Reference number: S15135; MUID:91378369
                                                                                                                                                    R.Collier, S.; Tassabehji, M.; Strachan, T.
Nature Genet. 3, 260-265, 1993
A;Title: A de novo pathological point mutation at the 21-hydroxylase locus: implicati
A;Reference number: IS8113; MUID:93251047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GDB:120605; OMIM:201910
A; Map position: 6p21.3-6p21.3
A; Introns: 67/1; 97/1; 148/3; 182/3; 245/3; 312/3; 372/2; 407/1
C; Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C; Keywords: chromoprotein: electron transfer; heme; iron; metalloprotein; monooxygena F; 288-450/Domain: cytochrome P450 homology <CYP>
F; 288-450/Domain: cytochrome P450 homology <CYP>
F; 428/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     benzphetamine N-demethylase (EC 1.14.14.-) cytochrome P450 2B - guinea pig (fragment)
                                                                                                                                                                                                                                                                                                                         A Accession: I58113
A Status: translated from GB/EMBL/DDBJ
A Status: translated to DNA
A:Residues: 109-171, N',173-185 <RE3>
A:Cross-references: GB:S60612; NID:9300314
C:Comment: Deficiency of this enzyme (21-hydroxylase deficiency) causes about 90 C;Genetics:
                          A;Molecule type: DNA
A;Residues: 149-182 <RE2>
A;Cross-references: GB:M19711; NID:g181289; PIDN:AAA83248.1; PID:g181290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.6%; Score 9; DB 1;
100.0%; Pred. No. 1;
Live 0; Mismatches
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100.0%; Pred. No. 1;
+ive 0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: GDB: CYP21; CYP21B
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Proc. Natl. Acad. Sci. U.S.A. 83, 2841-2845, 1986
A/Title: Complete nucleotide sequence of two steroid 21-hydroxylase genes tandemly arran A/Reference number: A00191; MUID:86206051
A/Reference number: A00191; MUID:86206051
A/Rocession: A00191
B/Rodigues: 1-425, PP, 427-494 <HIG>
B/Rodigues: 1-425, PP, 427-494 <HIG>
B/Rodigues: N.R.; Dunham, I.; Yu, C.Y.; Carroll, M.C.; Porter, R.R.; Campbell, R.D.
B/Rodigues: N.R.; Dunham, I.; Yu, C.Y.; Carroll, M.C.; Porter, R.R.; Campbell, R.D.
B/Rodigues: N.R.; Dunham, I.; Yu, C.Y.; Carroll, M.C.; Porter, R.R.; Campbell, R.D.
B/Rodigues: N.R.; Dunham, I.; Yu, C.Y.; Carroll, M.C.; Porter, R.R.; Campbell, R.D.
B/Rodigues: N.R.; Dunham, I.; Yu, C.Y.; Carroll, M.C.; Porter, R.R.; Chung, B.; Orlando, P.J.; Frisch, H.
B/Rodigues: N.R.; Dunham, I.; Yu, C.Y.; Carroll, M.C.; Dunham, I.; Yu, C.Y.; Carroll, M.C.; Campbell, R.J.; Miller, W.L.; Chung, B.; Orlando, P.J.; Frisch, H.
B/Rodigues: 1-9, T., 10-101, R., 10-3322, S.; 373-494 <ROD>
B/Rodigues: N.G.; Phillips III, J.A.; Miller, W.L.; Chung, B.; Orlando, P.J.; Frisch, H.
B/Rodession: A27865
B/Rodigues: 1-9, T.C., Tu-hydroxylase) gene deletions are not found in family studies A; Reference number: A3715; MUID:9129445; PIDN:AA59985.1; PID:9386993
B/Rodession: A3718
B/Rodession: A3718
B/Rodession: A3718
B/Rodession: A21889; MUID:9189446; PIDN:AA59985.1; PID:9386993
B/Rodession: A21889; MUID:9187288
B/Rodession: A21889; MUID:9187288
B/Rodession: A21889; MUID:9187288
B/Rodession: A21889; MUID:9187288
B/Rodession: A21889; BRAD Data Library, March 1991
B/Rodession: A21889; DATA A/Rodier, R.B.
B/Roberonce number: S26484
B/Rodession: A28649
B/Rodess
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A; Molecule type: DNA
A; Residues: 1-171, 'N',173-371 < HE2>
A; Cross-references: EMBL:X58898; NID:g30316; PIDN:CAA41702.1; PID:g30317
A; Accession: S29673
A; Accession: S29673
A; Molecule type: DNA
A; Residues: 1-9',L',10-101,'R',103-371 < HE5>
A; Cross-references: EMBL:X58900; NID:g30328; PIDN:CAA41704.1; PID:g30329
A; Cross-references: EMBL:X58900; NID:g30328; PIDN:CAA41704.1; PID:g30329
A; Cross-reference number: 139-144, 1988
A; Title: Nonsense mutation causing steroid 21-hydroxylase deficiency.
A; Reference number: 155547; MUID:88273565
A; Accession: 155547
A; Accession: 155547
A; Residues: 1-9',L',10-280,'L',282-494 < RES>
A; Residues: 1-9',L', 10-280,'L',282-494 < RES>
A; Amort M.; Parker, K.L.; Globerman, H.; New, M.I.; White, P.C.
R; Amort M.; Parker, K.L.; Globerman, H.; New, M.I.; White, P.C.
Proc. Natl. Acad. Sci. U.S.A. 85, 1600-1604, 1988
A; Title: Mutation in the CYPSIB gene (11e-172----Asn) causes steroid 21-hydroxylase defi
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A; Molecule type: DNA
A; Residues: 1-9,'L',10-101,'R',103-371 <HE4>
A; Cross-references: EMBL:X58902; NID:930325; PIDN:CAA41706.1; PID:930326
B; Helmberg, A.; Tabarelli, M.; Dobler, G.; Kofler, R.
Bibmitted to the EMBL Data Library, March 1991
A; Description: Identification of molecular defects causing congenital adrenal Hyperplasi
A; Reference number: S26584
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A;Cross-references: EMEL:X58904; NID:g30319; PIDN:CAA41707.1; PID:g30320
A;Accession: S29670
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A; Residues: 1-9,'L',10-101,'R',103-338,'H',340-452,'S',454-492,'S',494 <A
A; Cross-references: EMBL:X58906; NID:g30321; PIDN:CAA41709.1; PID:g30322
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Accession: 159109
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A Molecule type: protein
A; Residues: 1-33 <ARC>
A; Residues: 1-33 <ARC>
R; Yamada, H.; Kaneko, H.; Takeuchi, K.; Oguri, K.; Yoshimura, H.
Arch. Biochem. Biophys. 299, 248-254, 1992
A; Title: Tissue-specific expression, induction, and inhibition through metabolic inte
A; Reference number: $28205; MUID:93073973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Narimatsu, S.; Akutsu, Y.; Matsunaga, T.; Watanabe, K.; Yamamoto, I.; Yoshimura, H. Biochem. Biophys. Res. Commun. 172, 607-613, 1990
A;Title: Purification of a cytochrome P450 isozyme belonging to a subfamily of P450 I A;Reference number: A36154; MUID:91054472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: CYP2B
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: electron transfer; endoplasmic reticulum; heme; monooxygenase; oxidoreduc
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Gaps

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Indels

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C;Species: Vibrio cholerae (School and Paris) (C;Species: Vibrio cholerae (School and Paris) (C;Species: Vibrio cholerae (School and Paris) (C;Species: 18 - Nay-2000 #sequence_revision 20-Aug-2000 #sequence_revision 20-Aug-2000 #sequence_revision 20-Aug-2000 #sequence_revision 20-Aug-2000 #sequence_revision 20-Aug-2000 #sequence_revision W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. R;Heidelberg, J.F.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers 1, R.R.; Makalanos, J.J.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Estidues: 1-130 (LEV)
A; Estidues: 1-130 (LEV)
A; Experimental source: follicular lymphoma cells
A; Experimental source: follicular lymphoma cells
A; Experimental source: shown here is derived from the consensus nucleotide sequence of
b; Note: the sequence shown here is derived from the consensus nucleotide sequence of
c; Superfamily: immunoglobulin V region; immunoglobulin
C; Keywords: heterotetramer; hybridoma; immunoglobulin
C; Keywords: heterotetramer; hybridoma; immunoglobulin
C; Keywords: heterotetramer; hybridoma; immunoglobulin
F; 33-130/Product: Ig kappa chain V-I region CJ #status predicted <MAT>
F; 38-112/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA mismatch repair protein MutH VC0668 [imported] - Vibrio cholerae (strain N16961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833 A;Accession: D82294 A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RiLevy, S.; Mendel, E.; Kon, S.; Avnur, Z.; Levy, R.
J. Exp. Med. 168, 475-489, 1988
A;Title: Mutational hot spots in Ig V region genes of human follicular lymphomas.
A;Reference number: S04936; MUID:88316166
A,Title: Mutational hot spots in Ig V region genes of human follicular lymphomds. A;Reference number: $04936; MUID:88316166
A;Accession: $04936
A;Molecule type: mRNA
A;Residues: 1-125 <LEV>
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C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C;Accession: PL0113
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                            A.Cross-references: EMBL:X13076; NID:g33173; PIDN:CAA31477.1; PID:g736243 C.Superfamily: immunoglobulin V region: immunoglobulin homology C.Keywords: heterotetramer; immunoglobulin in E.1-17/Domain: signal sequence (fragment) #status predicted <SIG>F:18-125/Product: Ig kappa chain (fragment) #status predicted <MAT>
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tive 0; Mismatc)
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nes 8; Conservative
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Matches 8; Conserv
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Best Local S
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                                                                                                                                                                    District factor 4 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C;Accession: A26774; S45657
R;Doi, T.; Greenberg, S.M.; Rosenberg, R.D.
Mol. Cell. Biol. 7, 898-904, 1987
A;Title: Structure of the rat platelet factor 4 gene: a marker for megakaryocyte differe A;Reference number: A26774; MUID:87144262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M15254; NID:g206090; PIDN:AAA41832.1; PID:g206091
R;Ravanat, C.; Gachet, C.; Herbert, J.M.; Schuhler, S.; Guillemot, J.C.; Uzabiaga, F.; F
Eur. J. Biochem. 223, 203-210, 1994
A;Fitle: Rat platelets contain glycosylated and non-glycosylated forms of platelet factc
A;Reference number: 845657; MUID:94307262
A;Accession: S45657
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epididymis-specific four-disulfide core protein CE4 - dog
cyspecies: Canis lupus familiaris (dog)
Cyspecies: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 24-Oct-2000
CyAccession: 154768
CyRillerbrock, K.; Pera, 1.; Hartung, S.; Ivell, R.
Int. J. Androl. 17, 314-323, 1994
Artile: Gene expression in the dog epididymis: a model for human epididymal function.
A) Reference number: 154768; MUID:95263175
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C;Species: Homo sapiens (man)
C;Date: 28 Feb-1990 #sequence_revision 28 Feb-1990 #text_change 21-Jan-2000
C;Accession: S04936
C;Accession: S04936
J. Exp. Med. 168, 475-489, 1988
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C;Superfamily: antileukoproteinase; antileukoproteinase repeat homology
F;76-123/Domain: antileukoproteinase repeat homology <ALP>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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100.0%; Pred. No.
ive 0; Mismatch
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100.0%; Pre
0;
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A,Residues: 30-42 <RAV>
C,Superfamily: beta-thromboglobulin
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A; Residues: 1-105 <DOI>
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Best Local Similarity
8; Conserve
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A; Residues: 1-124 <ELL>
     11 LLLGLLLL 18
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A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337
A;Accession: A83458
                                      RESULT 11
A84458
hypothetical protein PA1509 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: A83458
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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Matches, 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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A;Gene: VC1265
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A;Residues: 1-221 <HEL>
A;Cross-references: GB:AE004153; GB:AE003852; NID:g9655103; PIDN:AAF93833.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
A;Genetics:
A;Genetics:
A;Genetico:
C;Superimental source: serogroup O2: strain N16961; biotype El Tor
C;Superimental source: serogroup O2: strain N16961; biotype El Tor
C;Superimental source: serogroup O3: strain N16961; biotype El Tor
C;Superimental source: serogroup O3: strain N16961; biotype El Tor
C;Superimental source: serogroup O3: strain N16961; biotype El Tor
C;Superimental source: serogroup O3: strain N16961; biotype El Tor
C;Superimental source: serogroup O3: strain N16961; biotype El Tor
C;Superimental source: serogroup O3: strain N16961; biotype El Tor
C;Superimental source: serogroup O3: strain N16961; biotype El Tor
C;Superimental source: serogroup O3: strain N16961; biotype El Tor
C;Superimental source: serogroup O3: strain N16961; biotype El Tor
C;Superimental source: serogroup O3: strain N16961; biotype El Tor
C;Superimental source: serogroup O3: strain N16961; biotype El Tor
C;Superimental source: serogroup O3: strain N16961; biotype El Tor
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S43455
S43455
S43455
S5245628: Pichia angusta
C;Species: Pichia angusta
C;Species: Pichia angusta
C;Date: 13-Jan-1995 #sequence_revision 23-Feb-1996 #text_change 20-Apr-2000
C;Accession: S43459
S;Agaphonov, M.O.; Poznyakovski, A.I.; Bogdanova, A.I.; Ter-Avanesyan, M.D.
A;Title: Isolation and characterization of the LEU2 gene of Hansenula polymorpha.
A;Reference number: S43454; MUID:95028149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tibonuclease S homolog - maize
N;Alternate names: S-like RNase
C;Species: Zea mays (maize)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C;Accession: T04095
R;Char, B.R.; Hake, S.
Submitted to the EMBL Data Library, August 1996
A;Reference number: 215206
A;Reference number: 215206
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Moceasion: T04095
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Cross-references: EMBL:U00889; NID:g392892; PIDN:AAA19110.1; PID:g392894
C;Genetics:
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100.0%; Pred. No. 8;
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100.0%; Pred. No. 5.1
tive 0; Mismatches
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100.0%; Pre/
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity
'-hea 8; Conserve
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270 LLLGLLLL 277
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A Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-380 <STO>
A; Cross-references: GB: AE004579; GB: AE004091; NID: g9947455; PIDN: AAG04898.1; GSPDB:GN
A; Experimental source: strain PAO1
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein VC1265 [imported] - Vibrio cholerae (strain N16961 serogroup O1) (Species: Vibrio cholerae (species: Na-Nag-2000 #sequence_revision 20-Aug-2000 #text_change O2-Feb-2001 (speciesion: A82220 #sequence_revision 20-Aug-2000 #text_change O2-Feb-2001 (speciesion: A82220 #sequence_revision 20-Aug-2000 #text_change O2-Feb-2001 (speciesion: A82220 #sequence of both chromosomes of the cholera pathogen Vibrio cholerae. As Accession: A82220
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Pypothetical protein - Deinococcus radiodurans (strain R1)
hypothetical protein - Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: F75257
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
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5. 9.6;
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100.0%; Pred. No. 9.6
tive 0; Mismatches
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G86587
heat shock protein-60 [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae 23-Mar-2001
C;Accession: G86587
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUD:20330349
A;Reference number: A86491; MUD:20330349
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-526 < STO>
A;Cross-references: GB:BA000008; NID:98979150; PIDN:BAA989985.1; GSPDB:GN00142
C;Genetics: Strain J138
C;Genetics: C;Genetics: Strain J138
C;Superfamily: Chaperonin groEL
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C.Species: Chlamydophila pneumoniae (Species: Chlamydophila pneumoniae)
C.Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C.Accession: D72036
Nature Genet. 21, 385-389, 1999
A.Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A.Reference number: A72000; MUID:99206606
A.Status: preliminary
A.Molecule type: DNA
A.Status: preliminary
A.Spoisoiles: 1-526 <ARN>
A.Status: DSA
A.Residues: 1-526 <ARN>
A.Res
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896
A;Accession: F75257
A;Status: preliminary
A;Molecule: type: DNA
A;Residues: 1-496 <WHI>A;Residues: 1-496 <WHI>A;Cross-references: GB:AEC02086; GB:AEC00513; NID:g6460395; PIDN:AAF12116.1; PID:g646046
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR2572
A;Map position: 1
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D72036
heat shock protein-60 - Chlamydophila pneumoniae (strain CWL029)
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100.0%; Pred. No. 11;
vative 0; Mismatches
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Best Local Similarity 100.0
المحمد 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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DB 2;
2.3%; Score 8; DB 2
100.0%; Pred. No. 11;
iive 0; Mismatches
Query Match 2.3
Best Local Similarity 100.
Matches 8; Conservative
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Gaps

Search completed: September 5, 2001, 10:57:14 Job time: 116 sec

us-09-457-066-43.Sep5oli.rpr

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APPLICANT: Brenner, Mitch
TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND ITS USE FOR
TITLE OF INVENTION: DRUG DEVELOPMENT FOR THE TREATMENT OF DISEASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                        Sequence Bequence Esquence Sequence Seq
                                                                                                                                                                                                                                                                                                              Sequence
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42.6%; Pred. No. 6.7e-11;
Live 16; Mismatches 38; Indels
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SOFTWARE: PatentIn Release #1.0, Version #1.30
US-08-795-430-11
US-08-024-868-2
US-08-242-097-2
US-09-245-297-2
US-09-26-695-2
US-08-242-097-6
US-09-206-695-6
US-09-206-695-6
US-09-042-105-2
US-09-042-105-2
US-09-042-105-18
US-08-795-430-8
US-08-795-430-8
US-08-795-430-13
US-08-795-430-13
US-08-795-430-13
US-08-795-430-13
US-08-795-430-13
US-08-999-251-27
US-08-999-251-27
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REGISTRATION NUMBER: 25,227
REFENCE/DOCKET NUMBER: 8389-031
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1155 Avenue of the Americas
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APPLICATION NUMBER: US/08/572,225
FILING DATE: 13-DEC-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08572225 Patent No. 5807981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Prockop, Darwin J. APPLICANT: Hojima, Yoshio APPLICANT: Li, Shi-Wu APPLICANT: Sieron, Aleksander APPLICANT: Brenner with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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Best Local Similarity 42.6
Matches 46; Conservative
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; MOLECULE TYPE: protein
US-08-572-225-1
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ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: New York
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      ADDRESSEE:
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      ; Search time 12.27 Seconds (without alignments) 578.946 Million cell updates/sec
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1848
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Sequence 2, A
Sequence 9, A
Sequence 22,
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Sequence 5,
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-021-287-3
US-08-866-650-5
US-08-866-650-5
US-08-866-650-5
US-08-866-650-5
US-08-836-008-2
US-08-936-135-2
US-08-936-135-2
US-08-936-135-10
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US-08-915-795-8
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US-08-915-795-9
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US-08-839-008-7
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                   protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length
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Scoring table:

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GENERAL INFORMATION:
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55 NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                        62 KFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV--EEPSDGSV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 LGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM--PQVTET-TSPS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 WGKFCGK-IAPSPVVSSGPFLFIKFVSD-YETHGAGFSIRYEIFKRGPECSQNYTAPT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67; Indels 34;
                                                                                                           114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/936,135
                                                                                                                                                                                                                                                                                             APPLICANT: Tessier-Lavigne, Marc
APPLICANT: He, Zhigang
APPLICANT: Chen, Hang
IIILE OF INVENTION: Semaphorin Receptors
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
9.1%; Score 169; DB 3;
Best Local Similarity 31.5%; Pred. No. 1.8e-09;
Matches 56; Conservative 21; Mismatches 67
                                                                                                                                                                                                                                 Sequence 6, Application US/08936135 Patent No. 6054293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 0097
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            923 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                       Patent No. 6054293
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94010
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COUNTRY:
                                                                                                                                                                                        RESULT 2
US-08-936-135-6
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US-08-866-650-3
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; Sequence 3, Application US/08866650

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55 NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV-EE 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Greenspan, Daniel S
APPLICANT: Greenspan, Razuhiko
APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUECES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Quarles & Brady
APPLICANT: Greenspan, Daniel S
APPLICANT: Greenspan, Kazuhiko
APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

8.9%; Score 165; DB 2;
Best Local Similarity 40.7%; Pred. No. 5.8e-09;
Matches 44; Conservative 21; Mismatches 35.
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                                                                                                                                             ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : Quarles & Brady
1 South Pinckney Street
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Patent No. 5981717
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 608-251-9166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1013 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-866-650-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                          CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Madison
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                                                                                                                                                                                                                                                       ZIP: 53703
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ZIP: 53703
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US-09-021-287-3
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55 NGSIHSPKFPHTYPRNMYLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
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                                                                                                                                                                                                                                                                Length 591;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              260 LSSESKLHGKFCGA-EVPEVITSQFNNMRIEFKSDNTV-SKKGFKAHF 305
                                                                                                                                                                                                                                                                                                     35; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
UNMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,650
                                                                                                                                                                                                                                                            8.8%; Score 162; DB 3;
ilarity 39.8%; Pred. No. 5.2e-09;
Conservative 22; Mismatches 35
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39.8%; Pred. No. 1.2e-08;
tive 22; Mismatches 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37094
FP: 960296.93839
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STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08866650 Patent No. 5939321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
                                                                                                  LENGTH: 591 amino acids
TYPE: amino acid
STRANDEDNESS: single
    610-407-0700
                                      TELEX: 846169
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                        610-407-0701
                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-991-408-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 53703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-866-650-5
                                                                                                                                                               linear
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3Y: linear
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 43; Conserv
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APPLICANT: Greensp
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      TELEPHONE:
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                        TELEFAX:
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US-08-866-650-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ARLETH, ANTHONY J.
APPLICANT: WILLETTE, ROBERT N.
APPLICANT: ELSHOURBAGY, NABIL A.
APPLICANT: LI, XIAOTONG
TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 165; DB 2;
Pred. No. 5.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FSASLEGO for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/991,408
                                                                                            PULICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/866,650
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960296.93839
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEPHONE: 608-251-5000
TELEPATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.9%; Score 165; DB Best Local Similarity 40.7%; Pred. No. 5.8e Matches 44; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                         APPLICATION NUMBER: US/09/021,287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60/034,471
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Patent No. 6008017
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23,031
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COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/03
FILING DATE: 02-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                          LENGIH: 1013 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-09-021-287-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19482
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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APPLICANT: ELSHOURBAGY, NABIL A.
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                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1013 amit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1013 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Hurle, Mark R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 39.8*
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-991-408-2
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                              USA
                                                                                                                                                                                                              ZIP: 19482
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                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-839-008-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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9
55 NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1013;
                                                         114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY 160
                                                                              114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35; Indels
                                                                                                                                                                             Sequence 5, Application US/09021287

Patent No. 5981717

GENERAL INFORMATION:

APPLICANT: Greenspan, Daniel S

APPLICANT: Takahara, Kazuhiko

TITLE OF INVENTION: Mammalian Tolloid-Like Protein

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady

STREET: 1 South Pinckney Street

CITY: Madison

STATE: WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/021,287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 8.8%; Score 162; DB 2; Best Local Similarity 39.8%; Pred. No. 1.2e-08; Matches 43; Conservative 22; Mismatches 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATFLLIC DATE:
FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/866,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/08991408; Patent No. 6008017; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WILLETTE, ROBERT N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARLETH, ANTHONY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1013 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-09-021-287-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                     RESULT 7
US-09-021-287-5
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US-08-991-408-2
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55 NGSIHSPKFPHTYPRNMYLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEF- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MCDonnell, Peter C
APPLICANT: MCNulty, Dean E
APPLICANT: Rosen, Craig A
APPLICANT: Storen, Craig A
APPLICANT: Young, Peter R
APPLICANT: Young, Peter R
APPLICANT: Yue, Tian-Li
TILE OF INVENTION: Smooth Muscle Cell-Derived Migration Factor
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.8%; Score 162; DB 3; Length 1013; 39.8%; Pred. No. 1.2e-08; tive 22; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY 160
APPLICANT: LI, XIAOTONG
TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/NA ....
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: SmithKline Beecham Corporation 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/034,471
FILING DATE: 02-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: ATG-500
TELEPHONE: 610-407-0700
TELEPHONE: 610-407-070
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224 AVSDDSRRLGKFCGD-AVPGSISSEGNELLVQFVSDLSVTAD-GFSASYKTLPRGTAKEG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 GSIHSPKFPHT-YPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV--- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 EEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                   PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.5%; Score 158; DB 2;
34.5%; Pred. No. 9.3e-09;
tive 21; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE CITY: HILLSBOROUGH CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/08936135
Patent No. 6054293
GENERAL INFORMATION:
APPLICANT: Tessier-Lavigne, Marc
APPLICANT: He, Zhigang
APPLICANT: Chen, Hang
TITLE OF INVENTION: Semaphorin Receptors
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UC97-288-2
                     23-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
PC-DOS/MS-DOS
                                                                                                                                           08/563,697
                                                                                                                                                                                                 NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFRENCE/DOCKET NUMBER: P503
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC
                              CURRENT MARK:

SUST MARKE:

APPLICATION NUMBER: US/08/
FILING DATE: 23-APR-1997
CLASSIFICATION DATA:

APPLICATION NUMBER: 08/563
FILING APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 -- POVTETTSPSV-LPPSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 OGPGPKRGTEPKVKLPPKS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy dis
                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 449 amino acids
                                                                                                                                                                                                                                                                                                        TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 34.5
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94010
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US-08-936-135-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              οy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 EEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM----- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smooth Muscle Cell-Derived Migration Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.5%; Score 158; DB 2; Length 449; 34.5%; Pred. No. 9.3e-09; tive 21; Mismatches 50; Indels
                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANUKESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                    PRIOR APPLICATION DATA.
APPLICATION NUMBER: 08/563,697
FILING DATE: 28-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50384
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,008
FILING DATE: 23-APR-1997
CLASSIFICATION: 435
                                                                                                IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HUIE, Mark R
APPLICANT: McDonnell, Peter C
APPLICANT: McNulty, Dean E
APPLICANT: Rosen, Craig A
APPLICANT: Siemens, Ivo R
APPLICANT: Young, Peter R
APPLICANT: Yue, Tian-Li
TILE OF INVENTION: Smooth Muscl
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08839008 Patent No. 5916758 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 -- PQVTETTSPSV-LPPSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282 QGPGPKRGTEPKVKLPPKS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 610-270-5090 INFORMATION FOR SEQ ID NO: 2:
                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.5%;
Best Local Similarity 34.5%;
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      449 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                  COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-839-008-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-839-008-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                94 FGLEDPEDDICKYDFVEVEEPSDGS--VLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFP 151
                                                                                                                                                                                                                                                                                                        7; Gaps
                                                                                                                                                                                                                                                                                                                                            34 SDKEQNGVQDPRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDER 93
                                                                                                                                                                                                                                                                                                                                                                                 16 SGHEVRSQQDPPCGGRPNSKDAGYITSPGYPQDYPSHQNCEWIVYAPEPNQKIVLNFNPH 75
                                                                                                                                                                                                                                                               Length 901;
                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                             coh 8.4%; Score 155.5; DB 3; 11 Similarity 32.8%; Pred. No. 5.3e-08; 43; Conservative 18; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tessier-Lavigne, Marc
APPLICANT: He, Zhigang
APPLICANT: Chen, Hang
TITLE OF INVENTION: Semaphorin Receptors
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24, Application US/08936135
Patent No. 6054293
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 05,627
REFERENCE/POCKET NUMBER: UC97
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-442
INFORDATION FOR SEQ ID NO: 24
SEQUENCE CHARACTERISTICS:
                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 901 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                906 amino acids
                                                                                                                                                single
                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-936-135-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 SEPGFCIHYSI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 QGAGFSLRYEI 141
                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                         TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94010
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                                                                                                                                                                                                                                                               Query Match
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76 FEIEKHD---CKYDFIEIRDGDSESADLLGKHCGN-IAPPTIISSGSVLYIKFTSD-YAR 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 FGLEDPEDDICKYDFVEVEEPSDGS--VLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFP 151
                                                                                                                            16 SGHEVRSQQDPPCGGRPNSKDAGYITSPGYPQDYPSHQNCEWIYYAPEPNQKIVLNFNPH 75
                                                                                              34 SDKEQNGVQDPRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDER 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 SDKEQNGVQDPRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDER 93
    Length 906;
                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,135
    DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.4%; Score 155.5; DB 3;
Best Local Similarity 32.8%; Pred. No. 5.4e-08;
8.4%; Score 155.5; DB 3 32.8%; Pred. No. 5.4e-08; tive 18; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: SCIENCE, & TECHNOLOGY LAW GROUP 75 DENISE DRIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/08936135
Patent No. 6054293
GENERAL INFORMATION:
APPLICANT: Tessier-Lavigne, Marc
APPLICANT: He, Zhigang
APPLICANT: Chen, Hang
TITLE OF INVENTION: Semaphorin Receptors
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-936-135-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: HILLSBOROUGH
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                           152 SEPGFCIHYSI 162
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  Query Match
Best Local Similarity
Matches 43; Conserv
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Search completed: September 5, 2001, 10:54:52
Job time: 49 sec
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOUTHWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/936,135 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.4%; Score 155.5; DB 3;
32.8%; Pred. No. 5.4e-08;
tive 18; Mismatches 63;
                                                                                                                                                                                     APPLICANT: Tessier-Lavigne, Marc
APPLICANT: He, Zhiqang
APPLICANT: Chen, Hang
APPLICANT: Chen, Hang
APPLICANT: Chen, Hang
NUMBER OF SEQUENCES: 26
CORRESPONDENCES: 26
CORRESPONDENCE ADDRESS:
STREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tessier-Lavigne, Marc APPLICANT: He, Zhigang APPLICANT: Chen, Hang TITLE OF INVENTION: Semaphorin Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18, Application US/08936135 Patent No. 6054293
                                                                                                                         Sequence 10, Application US/08936135 Patent No. 6054293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION UNDBER: 36,627
REFERENCE/DOCKET NUMBER: UC97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4341
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 999 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.4%
Best Local Similarity 32.8%
Matches 43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: peptide US-08-936-135-10
                                                                                                                                                                                                                                                                                                                                                               CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 SEPGFCIHYSI 162
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                   131 OGAGFSLRYEI 141
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                                                                                                                                                                     GENERAL INFORMATION:
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94 FGLEDPEDDICKYDFVEVEPSDGS--VLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 SRHQVRGQPDPPCGGRLNSKDAGYITSPGYPQDYPSHQNCEWIVYAPEPNQKIVLNFNPH 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 SDKEQNGVQDPRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDER 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 909;
                                                                                                                                                                                                                      OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pelease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.4%; Score 155.5; DB 3 32.1%; Pred. No. 5.4e-08; tive 20; Mismatches 62
                  ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: UC97-288-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEPAK: (650) 343-4341
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 909 amino acids TYPE: amino acid . STRANDEDNESS: single
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Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: peptide US-08-936-135-18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
                                          STREET: 75 DENISE CITY: HILLSBOROUGH
                                                                                    STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 SEPGFCIHYSI 162
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|131 QGAGFSLRYEI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                 94010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Wed Sep

OM protein - protein search, using sw model

5, 2001, 10:54:03 September ou:

; Search time 16.06 Seconds (without alignments) 1636.377 Million cell updates/sec

US-09-457-066-43 1848 Perfect score:

1 MLLLGLLLTSALAGQRTGT.....DVALEHHEECDCVCRGNAGG 345 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

219241

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\* Database

pir1:\* pir2:\* pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		đ			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
	191	10.3	707	5	JC2218	procollagen C-end
7	190	10.3	823		A58788	procollagen C-end
33	3	9.9	730		BMHU1	procollagen C-end
4	183.5	6.6	927	Н	JQ0948	A5 antigen precur
S	181	•	986		B58788	procollagen C-end
9	181		991		I49540	
7	174.5		3623		T09456	intrinsic factor-
80	160	8.7			T08618	intrinsic factor-
6	158	8.5			A55362	procollagen I C-p
10	153	8.3			A39288	ral
11	147.5	8.0			T30337	polyprotein - Afr
12	145.5	7.9			A59271	Ra-reactive facto
13	Ť	7.8			I54763	Ra-reactive facto
14	43.	7.8			S71352	metalloproteinase
15	141.5	7.7			T31069	tolloid-BMP-1 lik
16	140.5	7.6			T22812	hypothetical prot
17	139	7.5			T30549	hensin - rabbit
18	137.5	7.4			CIHURB	complement subcom
19	135.5	7.3	Н		S58984	ת ים
20	133.5	7.2			JH0403	procollagen I C-p
21	128	6.9			A41735	hyaluronate-bindi
22	127	6.9			869207	vascular endothel
23	125.5	6.8			TVCTSS	platelet-derived
24	125.5	6.8			T30018	hypothetical prot
25	123	6.7			JC6506	tumor necrosis fa
9₹	119.5	6.5	~		T42721	CRP-ductin-alpha
27	117.5	6.4			472	TSG-6 homolog PS4
28	117.5		1290		57	ebnerin precursor
29	114.5	6.2	200		151551	platelet-derived

platelet-derived g platelet-derived g complement subcomp platelet-derived g PDGF-related trans complement subcomp 16K vascular endot hypothetical prote UVS.2 protein - Af platelet-derived g platelet-derived g platelet-derived g platelet-derived g platelet-derived g	platelet-derived g	platelet-derived g
\$08220 151550 \$05008 \$05008 \$05008 \$05008 \$05554 \$05554 \$05097 \$25097 \$25097 \$25097 \$05097	JS0735	PFMSGB
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215 226 226 226 226 321 321 225 196 196	198	241
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114.5 114.5 1112.5 1112.5 1112.5 108.5 108.5 107 103.5 103.5	102.5	102.5
0 1 1 2 2 3 3 3 3 4 4 4 4 4 9 9 9 9 9 9 9 9 9 9 9	<b>4</b> 3	4.5

# ALIGNMENTS

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procollagen C-endopeptidase (EC 3.4.24.19) - African clawed frog (clone 22AN)
N.Alternate names: bone morphogenic protein 1
C.\$pecides: Xenopus laevis (African clawed frog)
C.\$Accession: JC2218
A;Reference number: JC2218; MUID:94085787
A;Recence number: JC2218; MUID:94085787
A;Recence number: JC2218; MUID:94085787
A;Recession: JC2218
A;Molecule type: mRNA
A;Residues: I-707 cAMBA
A;Residues: I-707 cAMBA
A;Residues: I-707 cAMBA
A;Cross-references: GB:L12249; NID:9406540; PIDN:AAA16313.1; PID:9406541
C;Comment: This protein induces ectopic cartilage formation in vivo.
C;Comment: This protein induces ectopic cartilage formation in vivo.
C;Comment: This protein induces ectopic cartilage formation in vivo.
C;Comment: This protein induces ectopic cartilage formation in vivo.
C;Superfamily: procollagen C-endopeptidase; ajvcoprotein; hydrolase; metalloproteinase; zinc F:393-294/Domain: astacin homology <AST>
F:285-394/Domain: clr/Cls repeat homology <CIRI>F:398-510/Region: complement Ir/1s-like repeat
F:398-510/Region: complement Ir/1s-like repeat
F:398-510/Region: complement Ir/1s-like repeat
F:554-666/Region: complement Ir/1s-like r

F;528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Gaps .. œ Length 707; 33; Indels 10.3%; Score 191; DB 2; 45.2%; Pred. No. 5.6e-08; tive 16; Mismatches 33; Local Similarity 45.2% les 47; Conservative Query Match Best Loca Matches

5,

55 NGSIHSPKFPHTYPRNMYLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113 g δλ

114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGF 156 õ

629 618 LTSDSKLHGKFCGS-ELPAVITSQYNNMRIEFKSDNTV-SKKGF

Db

# RESULT

mp ei in li li te ac ac

procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form HIS - human N;Alternate names: bone morphogenic protein splice form BMP-1/His C;Species: Homo sapiens (man) C;Date: 28-Mar-1998 #sequence\_revision 09-Apr-1998 #text\_change 18-Jun-1999 C;Accession: A37278; A58788 A58788

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C; Genetics:

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F.130-321/Domain: astacin homology <Asr>
F.322-431/Domain: Clr/Cls repeat homology <CIRI>
F.322-431/Domain: Clr/Cls repeat homology <CIRI>
F.351-544/Domain: Clr/Cls repeat homology <CIRI>
F.551-587/Domain: Clr/Cls repeat homology <CIRI>
F.551-700/Domain: Clr/Cls repeat homology <CIRI>
F.511-700/Domain: Clr/Cls repeat homology <CIRI
F.5
                                                                                                                                                                                       A,Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen t C;Superfamily: procollagen C-endopeptidase; astacin homology; Cir/Cis repeat homology C;Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; F;1-22,Domain: signal sequence #status predicted <SIG>
E;23-730/Product: procollagen C-endopeptidase splice form BMP1 #status predicted <MAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-927 <TRS: 1-9222963 
A; Experimental source: tadpole, brain ba moits homologous to complement components Clr and Cls and thing protein has moits homologous to complement components Clr and Cls and the neuronal C; Comment: This protein is a neuronal cell surface molecule involved in the neuronal C; Superfamily: Xenopus A5 antigen; Clr/Cls repeat homology; discoidin I amino-termina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Title: The A5 antigen, a candidate for the neuronal recognition molecule, has homol A,Reference number: JH0466; MUID:91337458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;214/Active site: Glu #status predicted F;565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| :||| | ||:||:|| || 655 LTADSKLHGKFCGS-EKPEVITSOYNNMRVEFKSDNTV-SKKGFKAHF-----FSEKR 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGSIHSPKFPHTYPRNMVLVWRLVANDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||| || :| || || :| :| || || 599 NGSITSPGWPKRYPTQ-YRISLQFD---FFETEGNDVCKYDFVEVRSG 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 VIISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLIFDERFGLEDPEDDICKYDFV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;861-883/Domain: transmembrane #status predicted <TMM>
F;150,261,300,523,844/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 730;
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C; Keywords: duplication; glycoprotein; transmembrane protein
F; 1-21/Domain: signal sequence #status predicted <SIG>F; 22-927/Product: A5 antigen #status predicted <A5A>F; 22-927/Product: A5 antigen #status predicted <A5A>F; 27-138/Domain: CII/Cis repeat homology <CIRI>
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F;274-424/Domain: discoidin I amino-terminal homology
F;430-584/Domain: discoidin I amino-terminal homology
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Pred. No. 2.5e-07
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A5 antigen precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
      A;Cross-references: GDB:125203; OMIM:112264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     646-812/Domain: MAM homology <MAM>
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38.98;
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Best Local Similarity 38.9%
Marches 49; Conservative
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                                                                     position: 8p21-8p21
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Best Local Si
Matches 55
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                                                                                              A;Title: Novel regulators of bone formation: molecular clones and activities.
A;Reference number: A37278; MUID:89072730
A;Recession: A37278
A;Accession: A37278
A;Accession: A37278
A;Accession: A37278
A;Cross-references: GB:M22488; NID:g179499; PIDN:AAA51833.1; PID:g179500
A;Cross-references: GB:M22488; NID:g179499; PIDN:AAA51833.1; PID:g179500
A;Cross-references: GB:M22488; NID:g179499; PIDN:AAA51833.1; PID:g179500
A;Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are encoda;Reference number: A58788; MUID:95096114
                  R.W.; Hew
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F; 1-22/Domain: signal sequence #status predicted <SIG>
F; 33-823/Product: procollagen C-endopeptidase splice form HIS #status predicted <MAT>
F; 310-321/Domain: astacin homology <AST>
F; 32-431/Domain: Clr/Cls repeat homology <CIRI>
F; 435-544/Domain: Clr/Cls repeat homology <CIRI>
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R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz., Science 242, 1528-1534, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form BMP1 - human N;Alternate names: bone morphogenic protein 1 (BMP1) C;Specias: Homo sapiens (man) C;Date: 16.Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999 C;Accession: A37278; E58788 R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, Science 242, 1528-1534, 1988
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A;Molecule type: mRNA
A;Residues: 703-823 <TAK>
A;Cross-references: GB:L35278; NID:g619423; PIDN:AAC41703.1; PID:g619424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.3%; Score 190; DB 1; 36.0%; Pred. No. 8.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;591-700/Domain: Clr/Cls repeat homology <ClR3>F;738-752/Region: histidine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLSGLELLLCPHALVDTVPA--PPSALHGD 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 -----SIIMPQVTETTSPSVLPPSSLSLD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GDB:125203; OMIM:112264
A;Map position: 8p21-8p21
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;551-587/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: GDB: BMP1; BMP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-730 <WOZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A37278
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Query Match

Matches

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predicted

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A; Gene: GDB: BMP1

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procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - mous
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Blood 91, 3593-3600, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor, cubilin: Molecular characte
                                                                         C,Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T09456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   His, His, Tyr) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2173 GHFCGSHASSTLFTSDNQMFVQFISDHSNEGQGFKIKYEAKSLACGGNVYIHDADSAGYV 2232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SPKFPHTYPRNMYLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE--PSD 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Map position: 10p12
C; Superfamily: unassigned EGF-related proteins; EGF homology
C; Superfamily: unassigned EGF-related proteins; EGF homology
C; Superfamily: unassigned EGF-related spredicted <SIG>
F; 1-24, Domain: signal sequence #status predicted <SIG>
F; 25-3623, Product: intrinsic factor-B12 receptor #status predicted <MAT>
F; 456-467, Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:L24755; NID:g439606; PIDN:AAA37306.1; PID:g439607
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              660 LTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQRTGTRAESNLSSK-----LQLSSD--KEQNGVQDPRHERVVTISGNGSIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intrinsic factor-B12 receptor Cubilin precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.8%; Score 181; DB 2;
42.6%; Pred. No. 5.9e-07;
tive 16; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: T09456
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-3623 < KOZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.4%; Score 174.5; DB 2
31.9%; Pred. No. 1.1e-05;
tive 26; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: The human intrinsic factor-vitamin B12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <C1R>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CKeywords: hydrolase, metalloproteinase; zinc F;135-326/Domain: astacin homology <AST> F;556-592/Domain: GEF homology <EGI> F;556-705/Domain: CIr/CIs repeat homology <CIR> F;712-47/Domain: EGF homology <EG2. F;718-74/Domain: EGF homology <EG2. F;218-74/Domain: EGF homology <EG2. P;218-74/Domain: EGF homology <EG2. P;218-74/Domain: EGF homology <EG2. P;219-74/Domain: EGF homology <EG2. P;219-74/Domain: EGF homology <EG2. P;219-74/Domain: EG1 = EG1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-991 <RES>
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Best Local 3
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BYS/189

BYS/189

BYS/189

Concession: A37218; BSS/189

Concession: A37218; MUD: BS/189

A.Rocession: BSS/189

A.Roc
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                                                                                      EV--EEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM--P 165
                                                                                                                                 NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                IKITSPSYLTSAGYPHSYPPSQRCEWLIQAPEHYQRIMINFNPHFDLEDRE----CKYDYV
                                                                                                                                                                                                                                                 166 QVTE--TTSPSVLP-----PSSLSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 181; DB 1;
; Pred. No. 5.9e-07;
16; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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nes 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Si
Matches 46;
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Gaps

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A Gene: GDB:PCOLCE
A; Cross-references: GDB:305468; OMIM:600270
A; Cross-references: GDB:305468; OMIM:600270
A; Map position: 7421.3-7422
C; Superfamily: CIr/CIs repeat homology
C; Keywords: extracellular protein; glycoprotein; pyroglutamic acid
F; 1-25-70main: signal sequence #status predicted <ART>
F; 37-146/Domain: CIr/CIs repeat homology <CIRI>F; 37-146/Domain: CIr/CIs repeat homology <CIRI>F; 37-146/Domain: CIr/CIs repeat homology <CIRI>F; 26/Modified site: pyrrolidone carboxylic acid (GIn) (in mature form) #status predicted F; 29, 431/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dorsal-ventral patterning protein tolloid (EC 3.4.24.-) - fruit fly (Drosophila melan dorsal-ventral patterning protein tolloid (EC 3.4.24.-) - fruit fly (Drosophila melan C; Species: Drosophila melanogaster C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 #Sphimell, M.J.; Fergusson, E.L.; Childs, S.R.; O'Connor, M.B. Call 67, 469-481, 1991
A; Title: The Drosophila dorsal-ventral patterning gene tolloid is related to human bo A; Reference number: A39288; MUID:92034970
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein tolloid; astacin homology; Clr/Cls r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 AVSDDSRRLGKFCGD-AVPGSISSEGNELLVQFVSDLSVTAD-GFSASYKTLPRGTAKEG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 EEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM----- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 LAGQRIGTRAESNLSSKLQLSSDKEQNGVQDPRHERV----VIISGNGSIHSPKFPHTYP 68
                                                                                                      NID:g642907; PIDN:AAA61949.1; PID:g642908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-1057 <SHI>
A;Cross-references: GB:M76976; NID:g157305; PIDN:AAA28491.1; PID:g157306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 GSIHSPKFPHT-YPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;787-896/Domain: CIr/CIs repeat homology <CIR4>
F;900-1013/Domain: CIr/CIs repeat homology <CIR5>
F;221,225,231,280/Binding site: zinc (His, His, His, Tyr) #status F;222/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C'Keywords: duplication; hydrolase; metalloproteinase; zinc F;135-329/Domain: astacin homology <AST>
F;35-464/Domain: Clr/Cls repeat homology <CIR1>
F;468-578/Domain: Clr/Cls repeat homology <CIR2>
F;585-520/Domain: Clr/Cls repeat homology <CIR2>
F;585-520/Domain: Clr/Cls repeat homology <CIR2>
F;547-740/Domain: Clr/Cls repeat homology <CIR3>
F;747-782/Domain: Clr/Cls repeat homology <CIR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 8.5%; Score 158; DB 2; Best Local Similarity 34.5%; Pred. No. 1.8e-05; Matches 48; Conservative 21; Mismatches 50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.3%; Score 153; DB 1;
Best Local Similarity 33.3%; Pred. No. 0.00014;
Matches 47; Conservative 28; Mismatches 54,
       A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Superfamily: dorsal-ventral patterning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: FlyBase:FBgn0003719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 -- PQVTETTSPSV-LPPSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282 QGPGPKRGTEPKVKLPPKS 300
                                                                                                      A; Cross-references: GB:L33799;
                                                                      <TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: FlyBase:tld
                                                                      644-1
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                                                                                                                                                                                                                                                                                                                           intrinsic factor-B12 receptor CUBILIN precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: 108618
R:Moestrup, S.K.; Kozyraki, R.; Kristiansen, M.; Kaysen, J.H.; Rasmussen, H.H.; Brault,
J. Biol. Chem. 273, 5235-524, 1998
A;Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies
A;Reference number: 216459; MUID:98148073
A;Gene: Complex number: 216459; MUID:98148073
A;Reference number: 316459; MUID:98148073
A;Reference number: 316459; MUID:98148073
A;Gene: CUBILIN
C:Superfamily: unassigned EGF-related proteins; EGF homology
C;Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane
F;1-20/Domain: signal sequence #status predicted <MAT>
F;43-164/Domain: EGF homology <EGF!>
F;43-164/Domain: EGF homology <EGF!>
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C;Accession: A55362
B;Takahara, K.; Kessler, E.; Biniaminov, L.; Brusel, M.; Eddy, R.L.; Jani-Sait, S.; Show J. Biol. Chem. 269, 26280-26285, 1994
A;Title: Type I procollagen COOH-terminal proteinase enhancer protein: identification, FA;Reference number: A55362; MUID:95014462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
975 SS-FYLEFHYN--CTNDYLEIXDTAAQTFLGRYCGK-SIPPSLTSNSNSIKLIFVSDSAL 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1142 KFKSDAALTAKGFSA------YWDGS--STGCGGN----LTTPTGVLTSPNYPM 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 DERFGLEDPEDDICKYDFVEVEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYF 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 AFS--TLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNLLKEEVKLY- 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 QLSSDKEQNGVQDPRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTF 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 PSEPGFCIHY-----SIIMPQVTET----TSPSVLP---PSS-----LSLDLLNNAVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 ----SCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.7%; Score 160; DB 2; Length 362
Best Local Similarity 26.8%; Pred. No. 0.00018;
Matches 90; Conservative 44; Mismatches 130; Indels
                                                                                                                                                 117 GSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1184 PYYHSSECYWRLEASHG-SPFELEFQDFHLEHHPSC 1218
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C; Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serin F;1-15/Domain: signal sequence #status predicted <SIG> F;1-44,445.686/Product: Rarreactive factor 2 #status predicted <MAT> F;19-134/Domain: Clr/Cls repeat homology <CIRI> F;142-180/Domain: Clr/Cls repeat homology <CIRI> F;142-293/Domain: Clr/Cls repeat homology <FRI> F;360-351/Domain: complement factor H repeat homology <FRI> F;360-351/Domain: complement factor H repeat homology <FRI> F;45-679/Domain: trypsin homology <TRY> F;45-679/Domain: trypsin homology <TRY> F;16-180,180-186,180-180,184-211,241-259,300-348,328-361,366-412,396-430,434-5 F;158/Modified site: erythro-beta-hydroxyasparagine (Assn) #status predicted F;481-444-445/Cleavage site: Arg-Ile (autolytic) #status predicted
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C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 16-Jun-2000
C;Accession: 154763; JN0883
R;Sato, T:, Endo, Y:; Matsushita, M.; Fujita, T.
Int. Immunol. 6, 665-669, 1994
A;Title: Molecular characterization of a novel serine protease involved in activation
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C;Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; complement facto
C;Keywords: beta-hydroxyasparagine; complement pathway; duplication; glycoprotein; hy
E;1-17/Domain: signal sequence #status predicted <SIG>
F;18-448,449-699/Poroduct: Ra-reactive factor #status predicted <MAT>
F;18-135/Domain: Clr/Cls repeat homology <ClR1>
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F;73:91,443-157,153-166,166-1181.185-212,242-266,301-349,322-352,367-414,397-432,436-5
F;159/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;448-449/Cleavage site: Arg-Ile (autolytic) #status predicted
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Biochem. Biophys. Res. Commun. 196, 1003-1009, 1993
A;Title: A new member of the C1s family of complement proteins found in a bactericida
A;Reference number: JN0883; MUID:94059062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ra-reactive factor (EC 3.4.21.-) 1 precursor - human N;Alternate names: mannose binding protein-associated serine proteinase 1 (MASP-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-214, (E', 236-284, G', 286-498, 'K', 500-542, 'K', 544-642, 'S', 644-699
A; Cross-references: DbBJ: D17525; NID: 9439712; PIDN: BARO4477.1; PID: 9439713
A; Experimental source: liver
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A,Gene: GDB:MASP1; GDB:CRARF; CRARF1; PRSS5, MASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEFP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.9%; Score 145.5; DB 1 30.8%; Pred. No. 0.00035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: 154763; MUID:94289349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vec.,
Best Local Similaric,
"...hes 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;143-181/Domain: EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-699 <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: I54763
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N;Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)
C;Species: Homo saplens (man)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 16-Jun-2000
C;Accession: A59271
R;Thiel, S; Vorup-Jensen, T.; Stover, C.M.; Schwaeble, W.J.; Laursen, S.B.; Poulsen, K. Nature 386, 506-510, 1997
A;Title: A second serine protease associated with mannan-binding lectin that activates can serine protease associated with mannan-binding lectin that activates can second serine protease associated with mannan-binding lectin that activates can second serine ont shown; not compared with conceptual translation
A; Accession: A59271
A; Residues: 1-686 c_JEN>
A; Residues: 1-686 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Species: Xenopus laevis (African clawed frog)
C.Species: Xenopus laevis (African clawed frog)
C.Species: Xenopus laevis (African clawed frog)
C.Species: Tay 13037
R.State: 22-0ct-1999 #sequence_revision 22-oct-1999
C.Accession: T30337
R.Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.
Submitted to the EMBL Data Library, March 1998
A.Specription: CDNA cloning of ovochymase, a chymotrypsin-like protease released from Xe
A.Specrance number: 220829
A.Accession: T30337
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: Preliminary; translated from African RNA
A.Wolecule type: mRNA
A.Wolecule type: mRNA
A.Kolecule type: mRN
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                                                                                                                                                                                       432 VSGEVITTQTSRMLLNYVNRNAAKGYRGFK-ARFEVVCGGDLKLTKDQSIDSPNYPMDYM 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV-EEP 114
                                                                                                                               RNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE--PSDGSVLGRWCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETTSPSVLPPSSLSLDLLNNA-VTAFSTLEELIRYLEPD----RWQVDL------DS
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llarity 28.7%; Pred. No. 0.00066;
Conservative 34; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                          GTVPGKQTSKGNHIRIRFVSD 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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613 IISPQWIL 620
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Best Local S
Matches 54
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-- PTTTQATTDETVVGSCGGRFGGTQGRVATPNY -- PNNYDND 507
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Job time: 73 sec
                                  508 LECVYVIEVEV----
                                                                             552 ---IDMKMCG 558
                                                           272 PGCLLVKRCG 281
 459 TTTISTTTPV-
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                                                          56 GSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEP- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --SDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM---PQVTE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----RYLEPDRWQVD 211
                                                                        29 GQIQSPGYPDSYPSDSEVTWN-ITVPDGFRIKLYF-MHFNLE--SSYLCEYDYVKVE--T 82
                                                                                                               116 DGSVLGRWCGSGTVPGKQT -----SKGNHIRIRFVSDEYFPSE---PGFCIHYSII 163
                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63;
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                     Length 699;
                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;339-446/Domain: CIr/CIs repeat homology <CIRL>
F;484-592/Domain: CIr/CIs repeat homology <CIR2>
F;190,194,200/Binding site: zinc (His) #status predicted
F;191/Active site: Glu #status predicted
                                         40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.8%; Score 143.5; DB 2; 23.2%; Pred. No. 0.00043; tive 48; Mismatches 81;
                  Query Match 7.8%; Score 144; DB 1; Best Local Similarity 34.7%; Pred. No. 0.00048; Matches 41; Conservative 19; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTSPSVLPPSSLSLDLLNNAVTAFSTLEELI----
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les 58; Conserv
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Best Local Si
Matches 58
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N'Alternate names: probable metalloprotease TBL-1
C; Species: Aplysia californica (California sea hare)
C; Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 18-Aug-2000
C; Accession: T31069
R; Liu, O.R.; Hattar, S.; Endo, S.; MacPhee, K.; Zhang, H.; Cleary, L.J.; Byrne, J.H.;
J. Neurosci. 17, 755-764, 1997
A; Title: A developmental gene (Tolloid/BMP-1) is regulated in Aplysia Neurons by trea A; Accession: T31069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:U57369; NID:g1899041; PID:g1899042; PIDN:AAC47485.1
C;Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; Clr/Cls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 LSLDLLUNAVTAFS----TLEELIRYLEPDRWQVD---LDSLYKPTWQLLGKAFLYGKK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 GSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQL----TFDERFGLEDPEDDICKYDFVEVE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 LDSLYKPTWQLLGKAFLYGKKSKVVNLNLLKEEVKLYSCTPRNFSVSIREELKRTDTIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 SKVVNLNLLKEEVKLYSC-----TPRNFSVSIREELKRTDTIFWPGCLL-----VKRCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    282 GNCACCLHNCN-----ECQC-----VPRKVTKK---YHEVLQLRPKTGVKGLHKS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          640 DHGCEHVCVNTLGSYECTCKIGYELHSDGKKCEKACGGYLDAPSGTISSPSFPDLYPPD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
7.7%; Score 141.5; DB 2; Length 1070;
Best Local Similarity 20.1%; Pred. No. 0.0013;
Matches 80; Conservative 49; Mismatches 110; Indels 159;
                                         --GRRVELDFIDFVLEDET--NCRWDSLSINLGDGIK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 --EPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----LTDVALEHHEEC 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1070 <LIU>
                                                                                                                                                                                                                                                                                                                                          T31069
tolloid-BMP-1 like protein 1 - California sea hare
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GenCore version 4.5 Copyright (c) 1993 · 2000 Compugen Ltd.
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OM protein - protein search, using sw model

5, 2001, 10:54:03; Search time 12.6 Seconds (without alignments) 937.948 Million cell updates/sec September Run on:

Title: Perfect score: Sequence:

US-09-457-066-43 1848 1 MLLGLLLLTSALAGQRTGT.....DVALEHHEECDCVCRGNAGG 345

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

	Description	P98070 xenopus lae	P28824 xenopus lae	P13497 homo sapien	P98063 mus musculu	O14786 homo sapien	Q9qwj9 rattus norv	nw snw	. P79795 gallus gall	strong	Q15113 homo sapien		O60462 homo sapien	_		P98064 mus musculu			P48740 h complemen	P00736 homo sapien		Q61398 mus musculu						-		P15156 mesocricetu	7	-		Q9y5y6 homo sapien
SUMMARIES	O.	BMP1_XENLA	NRP1_XENLA	BMP1_HUMAN	BMP1_MOUSE	NRP1_HUMAN	NRP1_RAT	NRP1_MOUSE	NRP1_CHICK	SPAN_STRPU	PCO1_HUMAN	NRP2_RAT	NRP2_HUMAN	NRP2_MOUSE	TLD_DROME	CRAR_MOUSE	MAS2_HUMAN	BP10_PARLI	CRAR_HUMAN	C1R_HUMAN	PCO1_RAT	PCO1_MOUSE	VEGC_MOUSE	BMPH_STRPU	TSG6_HUMAN	VEGC_HUMAN	PDGB_FELCA	TSG6_RABIT	PDGA_XENLA	CASP_MESAU	PDGB_HUMAN	VEGF_CAVPO	TSIS_SMSAV	ST14_HUMAN
	angth DB	707			991 1			923 1	914 1	616 1	449 1	925 1	931 1	931 1	1057 1	704 1	686 1	597 1	699 1	705 1	468 1	468 1	415 1	639 1	277 1	419 1	245 1	276 1	226 1	695 1	241 1	164 1	226 1	855 1
•	& Query Match Length	10.3			8.6	٠		9.1		8.8	8.5	8.4	8.4	8.4	8.3	8.0	7.9	7.8		٠	•	7.2	٠			6.9			6.2		•	0.9	٠	5.9
	Score	191	183.5	181	181	176	172	169	167	163.5	158	155.5	155.5	155.5	153	7	വ	144.5	144	137.5	136.5	133.5	132	130	128	127	125.5	117.5	114.5	113	112.5	111.5		109
	Result No.	1	7	3	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	58	30	31	32	33

P52585 orf virus (P49765 homo sapien	P42664 xenopus lae	Q95229 ovis aries	P04085 homo sapien	P20033 mus musculu	P34007 oryctolagus	P15692 homo sapien	P31240 mus musculu	P28576 rattus norv	P52584 orf virus (
VEGH_ORFN7	UVS2_XENLA	PDGB_SHEEP	PDGA_HUMAN	PDGA_MOUSE	PDGA_RABIT	VEGF_HUMAN	PDGB_MOUSE	PDGA_RAT	VEGH_ORFN2
~ ~			<b>~</b>	-	٦	Н	-	-	Н
148	514	241	211	211	213	215	241	204	133
5.9	9.0	9.9	9.9	5.6	5.5	5.5	5.5	5.5	5.4
108.5	104	103.5	103	103	102.5	102.5	102.5	102	100.5
34	36	38	36	40	41	42	43	44	45

# ALIGNMENTS

PRESENTED BY A PROPERTY OF STANDARD BY A PRO
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PROSITE; PS01187; EGF_CA; 1.
Growth factor; Cytokine; Repeat; Bone; Cartilage; Hydrolase; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Gaps
                                                                                                                                                                                                                                                                  EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takagi S., Hirata T., Agata K., Mochil M., Eguchi G., Fujisawa H.; "The A5 antigen, a candidate for the neuronal recognition molecule, has homologies to complement components and coagulation factors."; Neuron 7:295-307(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY). PRESUMED TO BE INVOLVED IN THE WISTON. SETWEEN THE OPTIC NERVE FIBERS AND THE VISIAL CENTERS. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: RETINAL GANGLION CELLS AND VISUAL CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                  (CATALYTIC) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33; Indels
                                                  Zinc; Calcium; Signal;
                                                                                                                                                          BONE MORPHOGENETIC PROTEIN METALLOPROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (PO N-LINKED (GLCNAC. . .) (PO N-LINKED (GLCNAC. . .) (PO 1169980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   618 LTSDSKLHGKFCGS-ELPAVITSQYNNMRIEFKSDNTV-SKKGF 659
                                                                                                                                                                                                                                                                                                                                                                    (BY
(BY
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01-DEC-1992 (Rel. 24, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
NEUROPILIN-1 PRECURSOR (A5 PROTEIN) (A5 ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY. SIMILARITY: CONTAINS 2 CUB DOMAINS. SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.3%; Score 191; DB 1;
45.2%; Pred. No. 3.2e-08;
tive 16; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                    ZINC (CATALYTIC)
                                                                                                                                                                                                                                                                                                                                                                                            (CATALYTIC)
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BY SIMILARITY.
BY SIMILARITY.
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ZINC
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                                                       EGF-like domain;
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MEDLINE-91337458; PubMed-1908252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80673 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 45.2%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
105
295
326
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326
562
707 AA;
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                                                     Metalloprotease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8355;
                                                                             Glycoprotein.
SIGNAL
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P28824;
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DISULFID
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NRP1_XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 VTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EV--EEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM--P 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 QVTE--TISPSVLP-----PSSLSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDS
                                                                                                                                                                                                                                                                                    Glycoprotein; Neurone; Signal; Repeat; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.9%; Score 183.5; DB 1; Length 928; 30.7%; Pred. No. 1.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF6B323B0A4C789D CRC64;
                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL) CUB 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.

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F5/8 TYPE C 2.
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                                                                                                                                                                                                                                                                                                                         NEUROPILIN-1.
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SIMILARITY: CONTAINS 1 MAM DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                    PROBABLE
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                                                                                                                                                                     Pfam; PF00431; CUB; 2.
Pfam; PF00754; F5_F8_type_C; 2.
Pfam; PF00629; MAM; 1.
                                                                                                                                                                                                                     PROSITE: PS00740; MAM_1; 1.
PROSITE: PS01180; CUB: 2.
PROSITE: PS01186; FA58C_1; 2.
PROSITE: PS01286; FA58C_2; 2.
PROSITE: PS50060; MAM_2; 1.
Transmembrane: Glycoprotein; Ne
                                                                                                                        EMBL; D10467; BAA01260.1; -.
                                                                                                                                                                                                            PRINTS; PR00020; MAMDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 9.99
Best Local Similarity 30.77
Matches 55; Conservative
                                                                                                                                               InterPro; IPR000859; -. InterPro; IPR000998; -.
                                                                                                                                                                                                                                                                                                                                                           928
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SIGNAL
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TRANSMEM
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CARBOHYD
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SEQUENCE
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BMP1_HUMAN
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                                                                                                                                                                                                                                                                                                                                                        TISSUE-Placenta;
PubMed=9500680;
Janitz M., Heiser V., Boettcher U., Landt O., Lauster R.;
"Three alternatively spliced variants of the gene coding for the human bone morphogenetic protein 1.";
J. Mol. Med. 76:141-146(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takahara K., Lyons G.E., Greenspan D.S.;
"Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld)
are encoded by alternatively spliced transcripts which are
differentially expressed in some tissues.";
J. Biol. Chem. 269:32572-32578(1994).
-!-FUNCTION: CLEAVES THE C-TERMINAL PROPEPTIDES OF PROCOLLAGEN I, II
AND II. INDUCES CARTILAGE AND BONE FORMATION.
-!- CATALYTIC ACTIVITY: CLEAVAGE OF THE C-TERMINAL PROPEPTIDE AT
ALA-|-ASP IN TYPE I AND II PROCOLLAGENS AND AT ARG-|-ASP IN TYPE
                                                                                                                                                                   "The C'proteinase that processes procollagens to fibrillar collagens is identical to the protein previously identified as bone morphogenic protein-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
-!- ENZYME REGULATION: ACTIVITY IS INCREASED BY THE PROCOLLAGEN C--
ENDOPEPTIDASE ENHANCER PROTEIN.
-!- ALTERNATIVE PRODUCTS: 6 ISOPORMS; BMP1-1, BMP1-2, BMP1-3 (SHOWN
HERE). BMP1-4, BMP1-5 AND BMP1-6; ARE PRODUCED BY ALTERNATIVE
             PROCOLLAGEN C-PROTEINASE) (PCP) (MAMMALIAN TOLLOID PROTEIN) (MTLD)
                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM BMP1-1).
MEDLINE-89072730; PubMed=3201241;
Wozney J.M., Rosen V., Celeste A.J., Mitsock L.M., Whitters M.J.,
Kriz R.W., Hewick R.M., Wang E.A.;
"Novel regulators of bone formation: molecular clones and
activities.";
BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.19) (BMP-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- TISSUE SPECIFICITY: UBIQUITOUS.
-i- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
-i- SIMILARITY: CONTAINS 5 CUB DOMAINS.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC
-i- METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
                                                                                                                                         Li S.W., Sieron A.L., Fertala A., Hojima Y., Arnold W.V., Prockop D.J.;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS BMP1-4; BMP1-5 AND BMP1-6).
                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 93:5127-5130(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 703-986 FROM N.A. (ISOFORM BMP1-3).
                                                                                                        SEQUENCE FROM N.A. (ISOFORM BMP1-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Placenta;
MEDLINE=95096114; PubMed=7798260;
                                                                                                                                                                                                                                                                                                                  Science 242:1528-1534(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U50330; AAA93462.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAA69975.1;
AAC41710.1;
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                                                                             NCBI_TaxID=9606;
                                                                                                                                 PubMed=8643539;
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Y08725; C
Y08725; C
L35279; A
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EMBL;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
DKDECSKDNGGCQQDCVNTFGSYECQCR -> EKRPALQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QEYNELKMEPQEVESLGETYDEDSIMHYARNTFSRGIFLDT
IVPKYEVNGVKPPIGQR -> VLHSSLLLLSCGSRNGASFP
CSLESSTHQALCWTGLFLRPSPFPRLPLAAPRTLRAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IN ISOFORM BMP1-4).

AMGSING (IN ISOFORM BMP1-4).

AMGGETTKINGSTISPEMPREYPPRINCIMOLY -> GCY

DLQVGKPLLMDRHCFRLSTHGPEMLGTALRG (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGF-LIKE 1, CALCIUM-BINDING (POFENTIAL).
CUB 3.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
CUB 4.
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MISSING (IN ISOFORM BMP1-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISOFORM BMP1-5)
MISSIMG (IN ISOFORM BMP1-5).
DKDECSKDNGGCQQD -> GGELFGLLGHPPRRP (IN ISOFORM BMP1-6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase;
                                                                                                                                                                                       Prémui Pro1400; Astacin; 1.

R Pfam; Pr00431; CUB; 5.

R Pfam; Pr0048; EGF; 2.

R PROSITE; PS00140; ASTACIN.

R PROSITE; PS00140; ASTACIN.

R PROSITE; PS0010; ASTARINC_PROTEASE; 1.

R PROSITE; PS0010; ASX_HYDROXIL; 2.

R PROSITE; PS01186; EGF_2; 2.

R PROSITE; PS01186; EGF_2; 2.

R PROSITE; PS01187; EGF_CA; 2.

R PROSITE; PS01187; EGF_AIRE AGRANTING SIGNAL; EGF_AIRE AGRANTI
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D -> N (IN REF. 4).
R -> S (IN REF. 4).
V; F89201913AC3CBEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BONE MORPHOGENETIC PROTEIN METALLOPROTEASE.
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(BY
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ZINC (CATALYTIC)
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InterPro; IPR000859;
                                                   InterPro; IPR000130;
InterPro; IPR000152;
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                                                    5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENZYME REGULATION: ACTIVITY IS INCREASED BY THE PROCOLLAGEN C-ENDOPERTIDAGE ENHANCER PROTEIN.

ENDOPERTIDAGE ENHANCER PROTEIN.

ENDOPERTIDAGE ENHANCER PROTEIN.

AND FILOR PLATE REGION OF THE HEVELS IN EMBRYONIC MATERNAL DECIDUUM AND FILOR PLATE REGION OF THE NEURAL TUBE. LESS IN DEVELOPING MEMBRANOUS AND ENDOCHONDRAL BONE, SUBMUCOSA OF INTESTINE, DERMIS SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 2 EGF-DAMAINS.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY MI2A (ZINC METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
                                                                             NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                        599 NGSITSPGWPKEYPPNKNCIWQLVAPTQ-YRISLQFD---FFETEGNDVCKYDFVEVRSG 654
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                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND II. INDUCES CARTILAGE AND BONE FORMATION.
CATALYTIC ACTIVITY: CLEAVAGE OF THE C-TERMINAL PROPEPTIDE AT
ALA-|-ASP IN TYPE I AND II PROCOLLAGENS AND AT ARG-|-ASP IN TYPE
                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.19) (BMP-1)
(PROCOLLAGEN C-PROTEINASE) (PCP) (MANMALIAN TOLLOID PROTEIN) (WILD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein-1 (BMP-1),
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Sciurognathi; Muridae; Murinae; Mus
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STRAIN=C57BL/6; TISSUE=Embryo;
MEDLINE=94229342; PubMed=8174772;
WHEDLINE=94229342; PubMed=8174772;
FURAGGAW M., Noboru S., Hogan B.L.M., Jones C.M.;
"Embryonic expression of mouse bone morphogenetic protein-1 (!which is related to the Drosophila dorsoventral gene tolloid encodes a putative astacin metalloendopeptidase.";
Dev. Biol. 163:175-183(1994).
                         Length 986;
                                                                                                                                   114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY 160
                                                                                                                                                   Indels
                      9.8%; Score 181; DB 1; Lr
42.6%; Pred. No. 3.2e-07;
tive 16; Mismatches 38;
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                                                                                                                                                                                                                                 991 AA
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                  Conservative
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                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
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MGD; MGI:88176; Bmp1
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                     Query Match
Best Local Similarity
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P98063;
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CUB 2.
EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
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014786; 060461;
30-MAY-2000 (Rel. 39, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
NEUROPILIN-1 PRECURSOR (VASCULAR ENDOTHELIAL CELL GROWTH FACTOR 165
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38; Indels
                                                                                                                                                                        Signal;
                                             PROSITE; PS0012; ZINC_ROTEASE; 1.
PROSITE; PS0018; 2.
PROSITE; PS00180; CUB; 5.
PROSITE; PS00021; BGF_1; FALSE_NEG.
PROSITE; PS01186; BGF_2; 2.
PROSITE; PS01187; EGF_0A; 2.
PROSITE; PS01187; EGF_0A; 2.
PROSITE; PS01187; EGF_0A; 2.
PROSITE; PS01187; EGF_0A; SINC; Cartilage; Imetalloprotease; EGF-like domain; Zinc; Calcium; S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (CATALYTIC)
(CATALYTIC)
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EGF-LIKE 2,
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                                PRINTS; PR00480; ASTACIN.
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PF000431; CUB; 5.
PF00008; EGF; 2.
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SIGNAL 1 2
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-!- SIMILARITY: OCNTAINS 2 CUB DOMAINS.
-!- SIMILARITY: CONTAINS 2 FS/8 TYPE C DOMAINS.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COEXPRESSION WITH KDR RESULTS IN INCREASED VEGF-165 BINDING TO KDR
AS WELL AS INCREASED CHEMOTAXIS. IT MAY REGULATE VEGF-INDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20309748; pubMed=10748121;
Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
Form of vascular endothelial growth factor (vegfs) and of placenta growth factor-2, but only neuropilin-2 functions as a receptor for the 145-amino acid form of Vegfs.";
J. Blol. Chem. 275:18040-18045(2000).
J. Blol. Chem. 275:18040-18045(2000).
J. Blol. Chem. 275:18040-18045(2000).
J. Blol. Chem. PERCEPTOR INVOLVED IN THE POWELOPMENT OF THE CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE POWELOPMENT OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS IT BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-165 ISOFORM OF VEGF AND VEGF-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soker S., Klagsbrun M.; "Identification of a natural soluble neuropilin-1 that binds vascular endothelial growth factor: In vivo expression and antitumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: THE SOLUBLE/SNRP1 ISOFORM BINDS VEGF-165 AND APPEARS TO INHIBIT ITS BINDING TO CELLS. IT MAY ALSO INDUCE APOPTOSIS BY SEQUESTERING VEGF-165. MAY BIND AS WELL VARIOUS MEMBERS OF THE SEMAPHORIN FAMILY. ITS EXPRESSION HAS AN AVERSE EFFECT ON BLOOD VESSEL NUMBER AND INTEGRITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE SOLUBLE/SNRPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gagnon M.L., Bielenberg D.R., Gechtman Z., Miao H.-Q., Takashima S.,
                                                                                                                                                                                                                                                                                                     Soker S., Takashima S., Miao H.-O., Neufeld G., Klagsbrun M.; "Neuropilin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor."; Cell 92:735-745(1998).
                                                                                                                                           "Neuropilin is a receptor for the axonal chemorepellent semaphorin
                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (MEMBRANE-BOUND ISOFORM), AND SEQUENCE OF 22-39
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; MEMBRANE-BOUND (SHOWN HERE)
                                                                                                                                                                                                                                                                                                                                                                                                                                (SOLUBLE/SNRP1 ISOFORM), AND SEQUENCE OF 22-31
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 97:2573-2578(2000)
                                                                       SEQUENCE FROM N.A. (MEMBRANE-BOUND ISOFORM) MEDLINE-97433084; Pubmed-9288753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20183929; PubMed=10688880;
                                                                                                                                                                                                                                                                                    MEDLINE=98188099; PubMed=9529250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Prostatic adenocarcinoma,
                                                                                                                   Z., Tessier-Lavigne M.;
                                                                                                                                                                                          Cell 90:739-751(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
EFP -> GIK (IN SOLUBLE/SNRPI ISOFORM)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.5%; Score 176; DB 1; Length 923; 32.6%; Pred. No. 7.8e-07;
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D -> H (IN REF. 2).
E -> D (IN REF. 2).
N; ADEADC4A849E5D57 CRC64;
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EXTRACELLULAR (POTENTIAL).
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Last annotation update)
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F5/8 TYPE C 2.
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24; Mismatches
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EMBL; AF018956, AAC51759.1; -.
EMBL; AF016050; AAC444.1; -.
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Pfam; PF00754; F5_F8_type_C;
Pfam; PF00629; MAM; 1.
                                                                                                                                                                                     PRINTS; PR00020; MAMDOMAIN.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FA58C_1; 2.
PROSITE; PS01286; FA58C_2; 2.
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                                              EMBL; AF145712; AAF44344.1;
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                                                                                                                   InterPro; IPR000998; -.
                                                                                InterPro; IPR000421; -. InterPro; IPR000859; -.
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923 AA;
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Matches 57; Conserv
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01-0CT-2000 (
01-0CT-2000 (
                                                                   MIM; 602069;
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922 AA; 103082 MW; CC6F82AD098B0F2E CRC64;

us-09-457-066-43.Sep5.rsp

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PROSITE; PS01180; CUB; 2.
   SEQUENCE
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Cell 90:753-762(1997).

Cell 90:753-762(1997).

CERDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE PORMATION OF CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE PORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT STEPS TO SEMAPHORIN 3A, THE PLGF-2 ISOPORM OF PGF, THE VEGF-165 ISOPORM OF VEGF AND VEGF-B. COEXPRESSION WITH KOR RESULTS IN INCREASED VEGF-165 BINDIA TO KDR AS WELL AS INCREASED CHEMOTAXIS.

CIT MAY REGULATE VEGF-INDUCED ANGIOGENESIS (BY SIMILARITY).

CIT SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CIT SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CIT SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.

CIT SIMILARITY: CONTAINS 2 FG/B TYPE C DOMAINS.

CIT SIMILARITY: CONTAINS 2 FG/B TYPE C DOMAINS.
                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NEUROPILIN-1 PRECURSOR (VASCULAR ENDOTHELIAL CELL GROWTH FACTOR 165
                                                                                                                           Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                   Ginty D.D.;
"Neuropilin is a semaphorin III receptor.";
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F5/8
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MEDLINE-97433085; PubMed-9288754;
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Pfam: PF00429; MAM; 1.
Pfam: PF00754; F5_F8_type_C; 2.
PRINTS; PR00020; MANDOMAIN.
PROSITE; PS01180; CUB; 2.
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                                                                 NCBI_TaxID=10116
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           RECEPTOR)
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CATRAIN—BALB/C; TISSUB—Embryonic brain;

MEDLINE—96353149; PubMed=8748368;

MEDLINE—96353149; PubMed=8748368;

A Kawakami A., Kitsukawa T., Takagi S., Fujisawa H.;

Rawakami A., Kitsukawa T., Takagi S., Fujisawa H.;

T "Developmentally regulated expression of a cell surface protein,

The moure pilin, in the mouse nervous system...;

J. Neurobiol. 29:1-17(1996)

C. I- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE

CARDIOVASCULAR SYSTEM, IN AMGIOGENESIS, IN THE FORMATION OF

CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS

SYSTEM. IT MEDIATES THE CHEWOREPULSANT ACTIVITY OF SERAPHORINS. IT

BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-165

INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS.

C. I SUBCELLUIAR LOCATION: TYPE I MEMBRANE PROTEIN.

C. I SIMILARITY: CONTAINS 2 CUB DOMAINS.

C. ISTAILARATTY: CONTAINS 2 EVB BYPE C DOMAINS.

C. ISTAILARATTY: CONTAINS 2 FS PROMAINS.
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                                                                                                                                                                                                                                                                 62 KFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV--EEPSDGSV 119
                                                                  Gaps
                                                                                                                                  2 LLLGLLLLTSALAGORTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHSP 61
                                                                                                                                                                                              7 LLCATLALALALAG------AFRSDKCGG-----TIKIENPGYLTSP 42
                                                                                                                                                                                                                                                                                                  120 LGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM--PQVTET-TSPS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                 100 WGKFCGK-IAPSPVVSSGPFLFIKFVSD-YETHGAGFSIRYEIFKRGPECSQNYTAPT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                  34;
Length 922;
                                                               67; Indels
   Score 172; DB 1;
Pred, No. 1.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             923 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence update)
                                                               21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence |
01-OCT-2000 (Rel. 40, Last annotation NEUROPILIN-1 PRECURSOR (A5 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR000421; Interpro; IPR000421; Interpro; IPR000859; Interpro; IPR000859; Pfam; PF00431; CUB; 2. Pfam; PF00754; F5_F8_type_C; 2. Pfam; PF00629; MAM; 1.
   9.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D50086; BAA08789.1; -. MGD; MGI:106206; Nrp.
                                                                  56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NRP1_MOUSE
P97333;
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Dev. Biol. 170:207-222(1995).
-!- FUNCTION: RECEPTOR INVOLVED.
CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE PORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-WHITE LECHORN; TISSUE-Embryonic brain;
MEDLINE-95324761; PubMed-7601310;
Takagi S., Kasuya Y., Shimizu M., Matsuura T., Tsuboi M., Kawakami A.,
Fujisawa H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 KFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV--EEPSDGSV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 LLCATLALALALAG-----TIKIENPGYLTSP 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 GYPHSYHPSEKCEMLIQAPEPYQRIIINFNPHFDLEDRD---CKYDYVEVIDGENEGGRL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHSP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 LGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM--PQVTET-TSPS 174
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                                                                                                                                                Neurone; Signal; Repeat; Receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0644BBA170796808 CRC64;
                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROBABLE.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 169; DB 1;
Pred. No. 2.9e-06;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-CT-2000 (Rel. 40, Last annotation update)
NEUROPILIN-1 PRECURSOR (A5 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             914 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 9.1%; Score 169; DB Best Local Similarity 31.5%; Pred. No. 2.9e Matches 56; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            F5/8 TYPE C 1.
F5/8 TYPE C 2.
                                                                                                                                                                                                                    NEUROPILIN-1
                                                                                                                                                                                                                                                                                        POTENTIAL
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                                                                                                                                            Pransmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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424
424
583
150
261
261
522
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923 AA;
                          PS01286; F
PS00740; N
PS50060; N
PS01285;
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P79795;
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DOMAIN
TRANSMEM
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CARBOHYD
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                                  PROSITE;
                                                                                                                                                                                     SIGNAL
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ID NRPI_C
AC 01-NOY
DT 01-NOY
DT 01-NOY
DT 01-NOY
DE NEUROP
OC GAILUS
OC ACIDOS
OC AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 EV--EEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM--P 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q.
                         SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: DEVELOPING NERVOUS SYSTEM; OPTIC TECTUM
TISSUE SPECIFICITY: DEVELOPING NERVOUS SYSTEM; OPTIC TECTUM
CLAYERS D AND E OF SGFS), AMACRINE CELLS OF RETINA, NEURITES OF
DORSAL ROOT GANGLIA. ALSO EXPRESSED IN NONBEURONAL CELLS, E.G.
BLOOD VESSELS IN THE ENTIRE EMBRYO.
SIMILARITY: BELONGS TO THE NURROPILLIN FAMILY.
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: CONTAINS 2 FS/8 TYPE C DOMAINS.
SIMILARITY: CONTAINS 1 MAM DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 ECSRNFTSSSGMIKSPGFPEKYPNSLECTYIIFAPKMSEIILEFESFE----LEPD 195
SIMILARITY). SEEMS TO HAVE CALCIUM-INDEPENDENT CELL ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neurone; Signal; Repeat; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 QVTE--TISPSVLP-----PSSLSLDL-----LNNAVTAFSTLEELIRYLEPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.0%; Score 167; DB 1; Length 914; 28.8%; Pred. No. 4.3e-06; Indels iive 31; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY.
SIMILARITY.
DD2EE6D6F0CBB68C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEUROPILIN-1.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
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F5/8
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BY
                                                                                                                                                                                                                                                                                         InterPro; IPR000421; -.
InterPro; IPR000959; -.
Pfam; PF00431; CUB; 2.
Pfam; PF00754; F5_F8_type_C; 2.
Pfam; PF00629; MAM; 1.
                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0020; MAMDOMAIN.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FA58C_1; 2.
PROSITE; PS01286; FA58C_2; 2.
PROSITE; PS00740; MAM_1; 1.
Transmembrane; Glycoprotein; Ne
                                                                                                                                                                                                                                                                             EMBL; D45416; BAA08256.1; -.
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Best Local Similarity 28.8
Matches 51; Conservative
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139
263
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422
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102
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204
273
429
914 AA;
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RESULT 9
SPAN\_STRPU

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Similarity

Best Local

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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                 Reynolds S.D., Angerer L.M., Palis J., Nasir A., Angerer R.C., "Early mRNAs, spatially restricted along the animal-vegetal axis of sea urchin embryos, include one encoding a protein related to tolloid
                                                                                                                Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                      Development 114:769-786(1992).
-!- TISSUE SPECIFICITY: ASYMMETRICALLY ALONG THE ANIMAL-VEGETAL AXIS
OF THE BLASTULA.
                                                                                                                                                                                                                                                                                                                   -! - DEVELOPMENTAL STAGE: VERY EARLY BLASTULA (BETWEEN 16-CELL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPKUUDUO,,
InterPro; IPKUUDUO,,
InterPro; IPRUUDIO66, -
Pfam; PF01400; Astacin; 1.
Pfam; PF00413; CUB; 2.
PRINTS; PR00480; ASTACIN.
PROSITE; PS00102; ZINC_PROTEASE; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01186; EGF_1; 1.
PROSITE; PS01186; EGF_2; FALSE_NEG.
Developmental protein; Repeat; Hydrolase; Protease; Zinc; Embryo; Metalloprotease; EGF-like domain; Signal.

1 16 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZINC (CATALYTIC) (BY SIMILARITY).

SINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ( SIMILARITY.
( SIMILARITY.
( SIMILARITY.
397CD923FFB9EB98 CRC64;
                                                                                                  Strongylocentrotus purpuratus (Purple sea urchin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARG/LYS-RICH (BASIC)
                          01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
SPAN PROTEIN PRECURSOR (EC 3.4.24.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METALLOPROTEASE
 616 AA
                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN. SIMILARITY: CONTAINS 2 CUB DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPAN PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGF-LIKE
                                                                                                                                                                                                    MEDLINE=92315921; PubMed=1618141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВҰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67902 MW;
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 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000130; -.
InterPro; IPR000561; -.
InterPro; IPR000859; -.
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                                                                                                                                             Strongylocentrotus.
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616 AA;
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                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  AND HATCHING)
                                                                                                                                                           NCBI_TaxID=7668;
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94
89
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295
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SPAN_STRPU
P98068;
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ACT_SITE
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TISSUE=Placenta;
MEDLINE=95014462; PubWed=7523404;
Takahara K., Kessler E., Biniaminov L., Brusel M., Eddy R.L.,
Jani-Sait S., Shows T.B., Greenspan D.S.;
Type I procollagen COOH-terminal proteinase enhancer protein:
identification, primary structure, and chromosomal localization of the
cognate human gene (FOCLCE).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Heart;
Hirahara I., Syoufuda K., Harada K., Tomita M., Urakami K., Terai H.,
Morisaki N., Saito Y.;
"Smooth muscle cell derived procollagen C-protease enhancer protein.";
Cell Struct. Funct. 21:662-662(1996).
                                                                                                                                                                                                                                                   439
                                                                                                                                                                                                                                                                                                                                                                                                                       PCO1_HUMAN STANDARD; PRT; 449 AA.
01513: 014550;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
9ROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR (PCPE) (TYPE I PROCOLLAGEN COOH TERMINAL PROTEINASE ENHANCER) (TYPE I PROCOLLAGEN COOH TERMINAL PROTEINASE ENHANCER) (TYPE I PROCOLLAGEN COOPTENASE ENHANCER)
                                                                                                                                                                                                              95 GLEDPEDDICKYDFVEVEEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPS-- 152
                                                                                    269 INSRL-GQRTALSAADIELANRIYECDDVEDCSNADECLNGGYHDADCDCVCPSSYSGDL 327
                     Gaps
                                                         LTSALAGQRTG-TRAESNLSSKLQLSSDKE-----QNGVQDPRHERVV--TISGN- 55
                                                                                                                                   94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gloeckner G., Scherer S., Schattevoy R., Boright A., Weber J., Tsui L.-C., Rosenthal A.; "Large-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUTLI loci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scott I.C., Clark T.G., Takahara K., Hoffman G.G., Greenspan D.S.; Structural organization and expression patterns of the human and mouse genes for the type I procollagen COOH-terminal proteinase enhancer protein.";
                                                                                                                                                         328 CQDGGPTVRPADCSYRFTEMTGEITSPNYPSNYEDNTACVYEIEG-PYGSTIELTF---L
                                                                                                                                                                                                                                  384 DMEIETETLCRYDAVEVRKDDINSIGEKECGN-TLPPVQISSSNQMAVSFTSD---PSIT
                                                                                                                                   -----GSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                   47;
5.1e-06;
thes 85; Indels
                                                                                                                                                                                                                                                                                         195
                                                                                                                                                                                                                                                                                         153 EPGFCIHYSIIMPQVT--ETTSPSVLPPSSLSLDLLNNAVTAFST
                                                                                                                                                                                                                                                                                                                            440 RRGFKATYVIIIQTTTVFSTTTLQTTPPSTTTLQTTNPSTTTLQT
28.0%; Pred. No. 5.16 ive 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 269:26280-26285(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jnpublished observations (FEB-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Placenta;
MEDLINE=99134301; PubMed=9933570;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reveals 17 genes.";
Genome Res. 8:1060-1073(1998).
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                   Conservative
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SEQUENCE FROM N.A.
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                     Matches
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                                                                                                          ΑN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Procedurate on proteolytic processing of procollagen C-terminal proteinase enhancer releases a metalloproteinase inhibitor.";
J. Biol. Chem. 275:1384-1390(2000).
I- BIOL. Chem. 275:1384-1390(2000).
I- FUNCTION: BINDS TO THE COOL-TERMINAL PROPEPTIDE OF TYPE I PROCOLLAGEN AND ENHANCES PROCOLLAGEN C-PROTEINASE ACTIVITY.
I- FUNCTION: C-TERMINAL PROCESSED PART OF PCPE (CT-PCPE) MAY HAVE AN METALLOPROTEINASE INHIBITORY ACTIVITY.
I- SUBCELLULAR LOCATION: SECRETED.
I- SUBCELLULAR LOCATION: SECRETED.
I- PTM: C-TERMINALLY PROCESSED AT MULTIPLE POSITIONS.
I- SIMILARITY: CONTAINS 1 UTR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 GSIHSPKFPHT-YPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV-- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 EEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM----- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20092917; PubMed-10625689;
Mott J.D., Thomas C.L., Rosenbach M.T., Takahara K., Greenspan D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLEAVAGE.

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

3D88430158648796 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                           PROCOLLAGEN C-PROTEINASE ENHANCER
                    PARTIAL SEQUENCE, AND CHARACTERIZATION OF INHIBITORY ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.5%; Score 158; DB 1;
34.5%; Pred. No. 9.7e-06;
live 21; Mismatches 50
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CUB 2.
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                                                                                                                                                                                                                                                      EMBL; L33799; AAA61949.1; ALT_SEQ.
EMBL; AB008549; BAA23281.1; -.
EMBL; AP053356; AAC78800.1; -.
EMBL; AF083655; AAD16041.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 QGPGPKRGTEPKVKLPPKS 300
                                                                                                                                                                                                                                                                                                    Interpro; IPR000859; -.
Interpro; IPR00134; -.
Fram: PF00431; CUB; 2.
Pfam: PF01759; NTR: 1.
PROSITE; PS01180; CUB; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47972
Genomics 55:229-234(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 34.5
Matches 48; Conservative
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29
431
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289
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329
287
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299
303
431
449 AA;
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                                                Banda M.J.;
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NRP2_RAT
ID NRP2_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                              PUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165 AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: FOUND IN CERTAIN NEURONAL POPULATIONS OF THE CNS AND IN OTHER NONNEURONAL TISSUES INCLUDING MESENCHYMAL TISSUE LINING IN THE RIBS.
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
NEUROPILIN-2 PRECURSOR (VASCULAR ENDOTHELIAL CELL GROWTH FACTOR 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97433085; PubMed=9288754;
Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neurone; Signal; Repeat; Receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LINING IN THE KIBS.
SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
SIMILARITY: CONTAINS 1 MAM DOMAIN.
                                                                                                                                                                                                                                                                                                                                                Ginty D.D.;
"Neuropilin is a semaphorin III receptor.";
Cell 90:753-762(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F5/8 TYPE C 1.
F5/8 TYPE C 2.
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CUB 2.
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InterPro; IPR000421; -.
InterPro; IPR000959; -.
InterPro; IPR000998; -.
Pfam; PF00431; CUB; 2.
Pfam; PF00629; MAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00754; F5_F8_type_C; 2. PROSITE; PS01180; CUB; 2. PROSITE; PS01285; FA58C_1; 2. PROSITE; PS01286; FA38C_2; 2. PROSITE; PS50060; MAM_2; 1.
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                                                                                                                                            Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SPRAGUE-DAWLEY;
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925 AA;
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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and for commercial

Usage by

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MIM; 602070;
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EMBL;
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NRP2_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20309748; PubMed=10748121;
A Gluzman-Pottorak Z., Cohen T., Herzog Y., Neufeld G.;
Gluzman-Pottorak Z., Cohen T., Herzog Y., Neufeld G.;
Gluzman-Pottorak Z., Cohen T., Herzog Y., Neufeld G.;
Torm of vascular endothelial growth factor (VEGF) and of placenta growth factor-2. but only neuropilin-2 functions as a receptor for the 145-amino acid form of VEGF.";
J. Biol. Chem. 275:18040-18045(2000).
C. !- FUNCTION: HIGH AFFLINTY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165
AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.
C. !- SUBGNIT: NEUROPILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH REUROPILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN 3C RECEPTOR.
C. !- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
C. !- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A22 (SHOWN HERE), A0 AND A17;
C. !- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A22 (SHOWN HERE), A0 AND A17;
C. !- ALTERNATIVE PRODUCTS SI SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS A0 AND A17).
MEDLINE=97470888; PubMed=9331348;
Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;
"Neuropilin-2, a novel member of the neuropilin family, is a high
affinity receptor for the semaphorins Sema E and Sema IV but not Sema
                                                                                                              QDPRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPED 101
                                                                                                                                                                                                       102 DICKYDFVEVEEPSDGS--VLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIH 159
                                                                                                                                                                                                                                    --CKYDFIEIRDGDSESADLLGKHCGN-IAPPTIISSGSVLYIKFTSD-YARQGAGFSLR 138
                                                                     Gaps
                                                                                                                                           060462; 014820; 014821; 014821; 01-0CT-2000 (Rel. 40, Created) 01-0CT-2000 (Rel. 40, Last sequence update) 01-0CT-2000 (Rel. 40, Last annotation update) NEUROPILIN-2 PRECURSOR (VASCULAR ENDOTHELIAL CELL GROWTH FACTOR 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soker S., Takashima S., Miao H.-O., Neufeld G., Klagsbrun M.; "Neuropilin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor."; cell 92:735-745(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRP2 OR VEĆF165R2.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                   7;
                   Length 925;
                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY. SIMILARITY: CONTAINS 2 CUB DOMAINS. SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS. SIMILARITY: CONTAINS 1 MAM DOMAIN.
                                           .9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    931 AA
                                                              19; Mismatches
                   Score 155.5;
Pred. No. 3.9
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                                                                   41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuron 19:547-559(1997).
              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Breast;
                                                                                                                                                                                                                                                                                                     160 YSI 162
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ID NRP2_HUMAN

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ID 01-0CT

DT 01-0CT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 SRHQVRGQPDPPCGGRLNSKDAGYITSPGYPQDYPSHQNCEWIVYAPEPNQKIVLNFNPH 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NRP2_MOUSE STANDARD; PRT; 931 AA.
035375; 035374; 035376; 035377; 035378;
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
REUROPILIN-2 PRECURSOR (VASCULAR ENDOTHELIAL CELL GROWTH FACTOR 165
RECEPPOR 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 155.5; DB 1; Length 931; Pred. No. 3.9e-05; Mismatches 62; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02 E -> K (IN REF. 1).
104830 MW; 270CBAE69A0A797C CRC64;
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N-LINKED (GLCNAC...) ()
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                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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F5/8 TYPE C 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
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Pfam; PF00529; MAM; 1.
Pfam; PF00754; F5_F8_type_C; 2.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FA58C_1; 2.
PROSITE; PS01286; FA58C_2; 2.
PROSITE; PS50060; MAM_Z; 1.
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                                                                              EMBL, AF022859; AAC51788.1; -. EMBL, AF022860; AAC51789.1; -. EMBL, AF016098; AAC12922.1; -.
                                                                                                                                                                 InterPro; IPR000859; -.
InterPro; IPR000998; -.
Pfam: profits
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2642
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2644
6744
6744
1105
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623
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633
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SIGNAL
1 2
CHAIN 21 93
DOMAIN 21 864
TRANSNEM 865 885
DOMAIN 890 931
DOMAIN 28 143
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208
277
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VARSPLIC
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                                            CARBOHYD
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DISULFID
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                                                                                                 Chen H., Chedotal A., He Z. G., Goodman C.S., Tessier-Lavigne M.; "Neuropilin-2, a novel member of the neuropilin family, is a high affinity receptor for the semaphorins Sema E and Sema IV but not Sema
                                                                                                                                             Neuron 19:547-559(1997).
                                                                                                                                                                AND VECE-145 ISOPORAS OF VEGE, AND THE PLGE-2 ISOPORAN OF PGE.
SUBUNTI: NETROPILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH
NEUROPILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN E RECEPTOR.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: 6 ISOPORAS; A22 (SHOWN HERE), A0, A5, A17,
BO AND B5; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING CNS, PNS AND IN SOME
NONNEURAL TISSUES INCLUDING LIMB BUDS, DEVELOPING BONES, MUSCLES,
INTESTINAL ENTHELLUM, KIDNEY, LUNG AND SUBMANNIBULAR GLAND.
IS DEVELOPMENTAL STAGE: THE EXPRESSION PATTERN IS VERY DYNAMIC AND
                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor; Alternative splicing.
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EXTRACELLULAR (POTENTIAL)
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                                                                  SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
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F5/8 TYPE C 2.
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                                                                                         MEDLINE=97470888; PubMed=9331348;
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Pfam; PF00754; F5_F8_type_C; 2.
Pfam; PF00652; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; F558C_1; 2.
PROSITE; PS01286; FA58C_2; 2.
PROSITE; PS01086; FA58C_2; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF022857; AAC53380.1; --
EMBL; AF022858; AAC53381.1; --
EMBL; AF022861; AAC53382.1; --
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864
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142
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427
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845
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175
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          Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000421;
                                            NCBI_TaxID=10090;
                                                                            STRAIN-BALB/C
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DOMAIN
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BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . . ) (POTENTIAL).

MISSING (IN ISOFORM A17).

MISSING (IN ISOFORM A5).

MISSING (IN ISOFORM A5).

EDEWUDPETHGEGSYEDETUDEYEGDWSNSSSTSGAGDP
SSGKEKSMLYTLDPILITIIAMSSLGVLLGATCAGLLYCT
CSYSGLSRSCTTLENYNELYDGATWYYWAAGGAVLVLAS

VALALVLHYHERYAAKTDHSITYKTSHYHOAPLAVEPT

LITKLEOPRGSHC (IN ISOFORM B0).

VDIPETHGGGSYEDEIDDEYEGDWSNSSSSTSGADPSGK
BKSMLYTLDPILITIIAMSSLGVLLGATCAGGLLLYCTCGSYS
GLSSRSCTTLENYNFELYDGLKHYNYLNHOKCCSEA. - S
GLSSRSCTTLENYNFELYDGLKHYNYLNHOKCCSES. - S
GLSSRSCTTLENYNFELYDGLKHYNYLNHOKCCSES. - S
GLSSRSCTTLENNYNFELYDGLWHYNYLNHOKCCSES. - S
GLSSRSCTTLENNYNFELYDGLWHYNYLNHOKCCSES. - S
GLSSRSCTTLENNYNFELYDDEN
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ALVLHYHRFRYAAKKTDHSITYKTSHYTNGAPLAVEPTLTI
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 FGLEDPEDDICKYDFVEVEVEEPSDGS--VLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFP 151
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Shimell M.J., Ferguson E.L., Childs S.R., O'Connor M.B.;
"The Drosophila dorsal-ventral patterning gene tolloid is related to
human bone morphogenetic protein 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 SGHEVRSQQDPPCGGRPNSKDAGYITSPGYPQDYPSHQNCEWIVYAPEPNQKIVLNFNPH 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLD_DROME STANDARD; PRT; 1057 AA.
P25723; 09VC46;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
DORSAL-VENYRAL PATTERNING TOLLOID PROTEIN PRECURSOR (EC 3.4.24.-).
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Finelli A.L., Bossie C.A., Xie T., Padgett R.W.;
"Mutational analysis of the Drosophila tolloid gene, a human BMP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 SDKEQNGVQDPRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDER
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G -> I (IN AAC53380 AND AAC53381).
7; 76F2443F411D2F63 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104558 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Development 120:861-870(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 32.89
Matches 43; Conservative
         427
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1157
629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        931 AA;
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PS00142; ZINC_PROTEASE; 1. PS01180; CUB; 5.
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33.3%;
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PRO0480; ASTACIN
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1057 AA;
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ACT_SITE
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CRAR_MOUSE
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   RAM MEDELINE—20196006; PubMed=10731132;

RAMIN ==EMERKELEY;

RAM MARIA ==EMERKELEY;

RA Amanatides P. G., Scherer S. E., Holf R. M., Hoskins R. A., Galle R. F.,

Radicon G. G., Celniker S. E., Li P. W., Hoskins R. A., Galle R. F.,

Radicon G. G., Wortman J. R., Yandlal M. D., Zhang O., Chen L. X.,

RA Brandon R.C., Rogers Y. H. C., Blazel R. G., Champe M., Ffeiffer B. D.,

RA Brandon R.C., Rogers Y. H. G., Blazel R. G., Champe M., Ffeiffer B. D.,

RADIL J. F., Agbayani A., An H. J., Andrews-Ffannkoch C., Baldwin D.,

RADIL J. F., Agbayani A., An H. J., Andrews-Ffannkoch C., Baldwin D.,

RADIL J. F., Agbayani A., An H. J., Andrews-Ffannkoch C., Baldwin D.,

RADICON R. W., Bouck J., Buck J., Brokstein P., Berchier B. M.,

RADICON R. J. Bouck J., Buck J., Brokstein P., Berchier B. M.,

RADICON R. J. Bouch D. A., Bulke C., Davenport L. B., Davies P. M.,

RADICON R. J. Candbiellan A. E., Garry N. S., Galbart W. Glasser K.,

ROSOR R., Joup L. E., Downes M., Dugan-Rocha S., Plukov B. C., Dunn P.,

RADICON R. J. Gabriellan A. E., Garry N. S., Galbart W. Glasser K.,

ROSOR R., Godyellic R., Howland T. J., Wernandez J. R. Houck J.,

RADIAL M., Kalush F., Kalren G. H., Karl, E. N. M. H. Houck J.,

Alalal M., Kalush F., Kalren G. H., Karl, E. N. M. Houck J.,

Lasko P., Lei Y., Levitsky A. A., Li J., Li Z., Liang Y., Lin Z.,

Lasko P., Lei Y., Levitsky A. A., Li J. J., Li Z., Liang Y., Lin X.,

RADICON G., Milshina N. V., Mobarry C., Morris J., Weinerla B.,

Radicon K. A., Mattei B., Marchob T. C., McLeod M. P., Morherson D.,

RADICAL M., Paltennes T. Simpson M., Stupski M. P., Smith H.O.,

RADICAL S. W., Wooden T., Weiner E., Wang S., Yang D.,

RADICAL S. W., Wooden T., Weiner C., Wang S., Yang O.,

RADICAL S. W., Woodenge T., Worley K.C., Wu D., Yang S., Yang O.,

RADICAN Spier E., Spradling S.C., Stapleton M., Stupski M. P., Sanith H.O.,

RADICAL S. W., Woodenge T., Worley K.C., Wu D., Yang S., Yang O.,

RADICAL S. W., Woodenge T., Weiner E., Wang S., Yang O.,

RADICAL S. R., Wooden W., Wallen D., S., Zabar D., Stang S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: REQUIRED FOR NORMAL DORSAL DEVELOPMENT. TLD MAY INTERACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- MISCELLANEOUS: MUTATIONS IN TLD GENE LEAD TO A PARTIAL TRANSFORMATION OF DORSAL ECTODERM INTO VENTRAL ECTODERM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
-!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 5 CUB DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHYSICALLY WITH DPP-C PROTEIN
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PIR, A39288; A39288.
HSSP; P00742; 1FAX.
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InterPro; IPR000130; -.
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Pfam; | Pfam; |

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PROSITE; PS01180; CUB; 5.
PROSITE; PS0010; ASX_HYDROXYL; 2.
PROSITE; PS00010; ASX_HYDROXYL; 2.
PROSITE; PS001186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 2.
Developmental protein; Hydrolase; Metalloprotease; Zinc; Glycoprotein; EGF-like domain; Calcium; Signal; Repeat; Zymogen.

27
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZINC (CAIALILLY) (DE SIGLIFALLI).
CELL ATTACHMENT SITE (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY
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Pred. No. 7.3e-05;
8; Mismatches 54; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
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SIMILARITY).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                           DORSAL-VENTRAL PATTERNING TOLLOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CATALYTIC) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76F4B5AEB7996FBA CRC64;
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ZINC (CATALYTI
BY SIMILARITY.
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28; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@illower.).
                                                                                                                                                                                                                                                                                                                                                                                              C4 COMPONENT BY CLEAVING THE ALPHA-CHAIN OF C4.
SUBUNIT: RARF CONSISTS OF A COMPLEMENT-ACTIVATING COMPONENT
CRARF) AND A POLLSACCHARIDE-BINDING (MANNOSE-BINDING) COMPONENT.
CRARF IS AN HETERODIMER OF A HEAVY (P70) AND A LIGH CHAIN (29)
LINKED BY A DISGLEIDE BOND.
                                                                                                                                                                                                                           Takayama Y., Takada F., Takahashi A., Kawakami M.; "A 100-kDa protein in the C4-activating component of Ra-reactive factor is a new serine protease having module organization similar to C1r and C1s.";
                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/C; TISSUE=Liver;
MEDLINE=93176166; PubMed=8439319;
Takahashi A., Takayama Y., Hatsuse H., Kawakami M.;
"Presence of a serine protease in the complement-activating component of the complement-dependent bactericidal factor, RaRF, in mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: LIVER.

DOMAIN: CRARF HAS A MODULE ORGANIZATION SIMILAR TO CIR AND CIS.

SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.

SIMILARITY: CONTAINS 2 CUB DOMAINS.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID=10090;
                                                                  PRECURSOR
                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
COMPLEMENT-ACTIVATING COMPONENT OF RA-REACTIVE FACTOR PRECURSC
(EC 3.4.21..) (RA-REACTIVE FACTOR SERINE PROTEASE P100) (RARF)
(MANNAN-BINDING LECTIN SERINE PROTEASE 1).
                                                                                                                                                                                                                                                                                                              SEQUENCE OF 465-704 FROM N.A., AND PARTIAL SEQUENCE
704 AA
                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00084; sushi; 2.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                 MEDLINE=94179811; PubMed=8133044;
                                                                                                                                                                                                                                                                                    Immunol. 152:2308-2316(1994).
                                                                                                                                                                                                     STRAIN-BALB/C; TISSUE=Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D16492; BAA03944.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR000561; -.
Interpro; IPR000859; -.
Interpro; IPR001254; -.
Interpro; IPR001314; -.
Interpro; IPR001881; -.
Pfam; PF00431; CUB; 2.
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; S01.198; -. MGD; MGI:88492; Maspl. InterPro; IPR000152; -. InterPro; IPR000436; -.
                                                                                                                       Mus musculus (Mouse)
                                                                                                           MASP1 OR CRARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P00736;
 CRAR_MOUSE
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205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 --RAAGNECPKLQPPVYGKIEPSQAVYSFKDQVLVSCDTGYKVLKDNGVMDTFQIECLKD 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS01186; CUB; 2.
PROSITE; PS01186: EGF_2; 1.
PROSITE; PS01187: EGF_CA; 1.
Hydrolase; Complement pathway; Serine protease; Protease; Glycoprotein; Sushi; Repeat; Signal; EGF-11ke domain; Hydroxylation.
                                                                                                                                                                      EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 CPYDYIKIKAGS--KWWGPFCGEKS-PEPISTQTHSVQILFRSDNSGENR-GWRLSY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 DRWQVDLDSLYKPTWQLLGKAFLYGKKSKVV-----NLNLLKEEVKLYSCTPRNFSVSI
                                                                                                                                                                                                                          SIMILARITY).
SIMILARITY).
SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 REELKRIDTIF------WPGCLLVKRCGGNCACCLHNCNECQCVPRKVTKKYHEVLQLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---LHNTTGVYTCSAHGTWTNKVL-KR---SLPTCLPVCG----VPKFSRKQISRIFNGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 GAWSNKI-----PTCKIVDCGAPAGLKHGLVTFSTRNNLTTYKSEIR-YSCQQPYYKM--
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N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
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                                                                                                   COMPLEMENT - ACTIVATING COMPONENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.0%; Score 147.5; DB 1; Length 7
22.5%; Pred. No. 0.00013;
Live 59; Mismatches 128; Indels
                                                                                                                RA-REACTIVE FACTOR (P100).
70 KDA CHAIN OF P100 (P70)
29 KDA CHAIN OF P100 (P29)
                                                                                                                                                                                                                          CHARGE RELAY SYSTEM (BY S CHARGE RELAY SYSTEM (BY S CHARGE RELAY SYSTEM (BY S PURDROXYLATION (POTENTIAL)
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Best Local Similarity 22.5.
A 75; Conservative
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183
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704 AA;
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SIGNAL
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CARBOHYD
SEQUENCE
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18;

5, 2001, 10:56:05

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091674 xenopus lae 097270 homo sapien 095570 homo sapien 096051 paracentrot 026051 paracentrot 096050 cyprinus ca 096900 cyprinus ca 0969072 triakis scy
                   057382 xenopus lae
043897 homo sapien
070244 rattus norv
091025 canis famil
091025 homo sapien
091026 homo sapien
091027 rattus norv
091072 rattus norv
091359 rattus norv
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091359 rattus norv
091674 xenopus lae
09qx38 rattus norv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tasic County Tasic True R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.; "CDNA cloning of fallotein from mouse ovary."; "CDNA cloning of fallotein from mouse ovary."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AFI1/608; ARE2516.1; -. InterPro; IPR0000859; -. InterPro; IPR0000859; -. Prosite; PS001180; CUB; 1. PROSITE; PS01180; CUB; 1. SMART; SM0042; CUB; 1. SEQUENCE 345 AA; 38741 MW; 3A58AIF701B84EA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 345;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
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          Q62381
O57382
O43897
Q9NQS4
O70244
Q9TU53
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Q01654
Q91674
Q9Y270
Q9S570
Q9UF09
Q26051
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09H2E4
09H2D5
09H2D5
09H2E3
09H2E3
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O09020
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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TISSUE-OVARY;
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RESULT
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1852.485 Million cell updates/sec
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                                                                                                                                                      1 MLLLGLLLLTSALAGQRTGT.....DVALEHHEECDCVCRGNAGG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                               425026 seqs, 132305027 residues
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Maximum Match 100%
Listing first 45 summaries
                                                          OM protein - protein search, using sw model
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Q9UL22
Q9UR41
Q91841
Q9EQT1
Q9GZP0
057658
Q91925
O57381
Q9UQ00
Q9VWM6
Q9Z135
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
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sp_phage:*
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length: 2000000000
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Gaps

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61 PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEFSDGSVL 120

61 PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL 120

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060494 057460 Q9DER7

Q9H2E1

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Result ě 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS 180

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61 PKFPHTYPRNTYLVWRLVAVDENVRIQLTFDERFGLEDPEDDLCKYDFVEVEEPSDGSVL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
SECRETORY GROWTH FACTOR-LIKE PROTEIN FALLOTEIN (SPINAL CORD-DERIVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUB-UTERUS;
TSai Y.J., Lee R.K.K., Lin S.P.;
"Fallotein, a novel growth factor like gene identified in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
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EMBL; AB033830; BAB19969.1; -.
SEQUENCE 345 Aa; 38734 MW; F296DA6E9B765D10 CRC64;
                                                                                                                                                                                                                                                                            STRAIN-WISTAR, TISSUE-KIDNEY,
Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
"Molecular Cloning of SCDGF-B, a Novel Growth Factor
                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 VTKKYHEVLQLRPKIGVKGLHKSLTDVALEHHEECDCVCRGNTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                        97.5%; Score 1801; DB 11; 96.8%; Pred. No. 6.2e-155;
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                                                      PRT;
                                                                                                                                          SPINAL CORD-DERIVED GROWTH FACTOR.
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                                                                                                                                                                                                                                                                                                                                    SCDGF/PDGF-C/fallotein.";
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                                                      PRELIMINARY;
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                                                                                                        (TrEMBLrel.
                                                                                                                                                                            Rattus norvegicus (Rat)
                                                                                                                          (TrEMBLrel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                      01-MAR-2001
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01-MAR-2001
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01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                            RSCDGF
                                                      O9EOX6
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GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS 180
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                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                      LKEEVKLYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=SWISS-WEBSTER/NIH;
Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
"The mouse Pdgfc gene: Dynamic expression in embryonic tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 345;
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                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PLATELET-DERIVED GROWTH FACTOR C.
                                                                                                                                                                         301 VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG
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Pred. No. 1.5e-156;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                   345
                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00042; CUB; 1.
SEQUENCE 345 AA; 38886 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.4%;
98.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mech. Dev. 0:0-0(2000).
EMBL; AF286725; AAF91483.1;
InterPro; IPR000072; -.
InterPro; IPR000859; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                        musculus (Mouse).
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Best Local S
Matches 341)
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Length 345; Indels

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RESULT Q9JHV8

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Gaps

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Length 345; Indels 9 9 180

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                                                                                                                                                                                                   590889CEA55CC5EA CRC64;
                                                                                                                                                                                                                                                                                    90.0%; Score 1664; DB 4;
86.7%; Pred. No. 1.6e-142;
tive 28; Mismatches 18;
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InterPro; IPR000072; -.
InterPro; IPR000859; -.
Pfam; PF00341; PDGF; 1.
Pfam; PF00431; CUB; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS02078; PDGF_2; 1.
SMART; SM0042; CUB; 1.
SEQUENCE 345 AA; 39043 MW; 5
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80.3%;
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 86.73
Matches 299; Conservative
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Best Local Similarity
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SEQUENCE
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                                                                                                          TISSUE-BRAIN;
MEDLINE=20317014; PubMed=10858496;
MEDLINE=20317014; PubMed=10858496;
Hamada T., Ui-Tei K., Miyata Y.;
"A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VEGF family.";
FEBS Lett. 475:97-102(2000).
EMBL; ARF001434; ARF00049.1; -...
EMBL; AB033831; BAB03266.1; -...
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Nat. Cell Biol. 0:0-0(2000).

EMBL, AF244813; AAF80597.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.2%; Score 1667; DB 4; Length 3
87.0%; Pred. No. 8.4e-143;
ive 27; Mismatches 18; Indels
                                to the EMBL/GenBank/DDBJ databases.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PLATELET-DERIVED GROWTH FACTOR C.
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                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000072; -.
InterPro; IPR000072; -.
Ffam; PF00341; PDGF; 1.
Pfam; PF00431; CUB; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS001280; CUB; 1.
SMART; SM0042; CUB; 1.
SEQUENCE 345 AA; 39029 MW; C
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                             Submitted (SEP-1998)
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                                                                                   SEQUENCE FROM N.A.
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uterus.";
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SEQUENCE FROM N.A.
STRAIN=WHITE LEGHORN; TISSUE=SPINAL CORD;
MEDLINE=20317014; PubMed=10858496;
MEDLINE=20317014; PubMed=10858496;
MEMDLINE=20317014; PubMed=10858496;
"A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VEGF family.";
FEBS Lett. 475:97-102(2000).
FEBS Lett. 475:97-102(2000).
InterPro; IPR000072; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 345;
301 VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97ACEA992BF5128C CRC64;
                                                                                                                                                                                                                                                                                     (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
                                 301 VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1552; DB 13;
Pred. No. 2.2e-132;
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RESULT
O90NRA1
LD 009
DT 001
DD 01
DD 01
DD 02
DD 02
DD 03
DD 03
DD 04
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Similarity
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                     NCBI_TaxID=9606;
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057658;
01-JUN-1998 (
                                                                                                                                              HSCDGF-B
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
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                                                            PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEFFSDGSVL 120
                                                                                                                                                                                              PGFCIHYSII---MPQ-----VTET-----TSPSVLPPSSLSLDLLNNAVTAFST 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEDPEDDICKYDFVEVEEPSDGS - - VLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSE 153
                       9
                                           9
   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          to
                      MLLLGLLLLTSALAGQRTGTRAESNLSSKLOLSSDKEQNGVQDPRHERVVTISGNGSIHS
                               GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS
                                                                                                                                            181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
                                                                                                                                                        LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQNGVQD-PRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 VEDLLKYFNPASWQDDLENLYMDTPRYRGRSY-HERKSK-VDLDRLNDDVKRYSCTPRNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVSIREBLKRIDIIFWPGCLLVKRCGGNCACCLHNCNECQCVPRKVTKKYHEVLQLRP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNLLKEEVKLYSCTPRNF
                                                                                                                                                                                                                                                                                                                                                                                                                 EEQUENCE FROM N.A.
Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
Hamedeular Cloning of SCDGF-B, a Novel Growth Factor Homologous SCDGF/PDGF-C/Fallotein.";
Blochem Blophys. Res. Commun. 0:0-0(2000).
EMBL; AB052170; BAB18920.1; -.
SEQUENCE 370 AA; 42809 MW; 7BE8A251F679BF73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.8%; Score 754; DB 11; Length 370;
46.2%; Pred. No. 4.1e-60;
tive 62; Mismatches 86; Indels 2
   Indels
                                                                                                                                                                                                                           VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
   31;
  37; Mismatches
                                                                                                                                                                                                                                                                                                  Ą
                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Last see 01-MAR-2001 (TrEMBLrel. 16, Last and SPINAL-CORD DERIVED GROWTH FACTOR-B.
                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 16, TrEMBLrel. 16, (TrEMBLrel. 16,
Matches 277; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Simi
hes 151;
                                                                                                                                                                                                                                                                                                         Q9EQT1;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                          RSCDGF-B.
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Matches
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TISSUE-AORTA;
Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu B., Liu Y.Q., Wang X.Y., Zhang C.L., Zhang J., Wei Y.J.,
Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
Cao H.O., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB033832; BAB18903.1; -.
EMBL; AR113216; AA339287.1; -.
EMBL; AR113216; AA339287.1; -.
EMBL; AR113216; AA339287.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEDPEDDICKYDFVEVEEPSDGSVL--GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGFCIHYSII---MPQVTETT------SPSVLPPSSLSLDLLNNAVTAFST 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNLLKEEVKLYSCTPRNF 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
"Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 EQNGVQD-PRHERVYTISGNGSIHSPKFPHTYPRNMYLVWRLVAVDENVRIQLTFDERFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGFKIYYSLLEDFQPAAASETNWESVTSSISGVSYNSPSVTDP-TLIADALDKKIAEFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRKVTKKYHEVLQLRP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                         01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation updat
SPINAL CORD-DERIVED GROWTH FACTOR-B (MSTP036).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 752; DB 4;
; Pred. No. 6.3e-60;
59; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCDGF/PDGF-C/fallotein.";
Biochem. Biophys. Res. Commun. 0:0-0(2000)
                                                                                                                                                                                                      370
314 -KTGVKGLHKSLTDVALEHHEECDCVC 339
                                 338 FKRRGKAKNMALVDIQLDHHERCDCIC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314 -KTGVKGLHKSLTDVALEHHEECDCVC 339
                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 IKRRGRAKTMALVDIQLDHHERCDCIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 148; Conservative
                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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EMBL; D83476; BAA11922.1;
HSSP; P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calcium-binding;
                                                  MEROPS; M12.015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            057381;
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O57381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWART; SM00042; CUB; 1.
Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   560 NGSISSPGWPRDYPPNKHCVWQLVAPTQ-YRISLRFD---FFETEGNDVCKYDFVEVRSG 615
                                                                                                 Eukaryoća; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                   Reynolds S.D., Puzas J.E., O'keefe R.J., Rosier R.N., Reynolds P.R.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases. EMBL: U7331; AAC02259.1; -. HSSP: P00736; 1APQ.
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.4%; Score 192.5; DB 13; Length 691; 38.6%; Pred. No. 6.3e-09; Live 21; Mismatches 46; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   691 AA; 77843 MW; 01245982B8DC8F28 CRC64;
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01-NOV-1996 (TrEMBLrel.-01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
BONE MORPHOGENETIC PROTEIN 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR001506; -.
Interpro; IPR001801; -.
Pfam; PF00431; CUB; 3.
Pfam; PF00431; CUB; 3.
Pfam; PF00400; Astacin; 1.
PRINTS; PF00400; ASTACIN.
PROSITE; PS01010; ASX_HYDROXYL; 1.
PROSITE; PS01180; CUB; 3.
PROSITE; PS01180; EGF_Z; 1.
PROSITE; PS01187; EGF_CA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           977 AA
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Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 38.69 les 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                          Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000130; -.
InterPro; IPR000152; -.
InterPro; IPR000561; -.
InterPro; IPR000859; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. TISSUE=EMBRYO;
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 PSVLPPS 179
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671 PPQIPPA 677
                                                                                                                                                                              NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                            MEROPS; M12.005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Q91925;
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DDR RRW DDR RW D
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nding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
977 AA; 110199 MW; 4D7D2E37C64FDFIF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 977;
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DBV. Biol. 0:0-0(0).
EMBL; Y09660; CAA70853.1; --
HSSP; P007765; JAPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
BONE MORPHOGENETIC PROTEIN 1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.3%; Score 191; DB 13; Best Local Similarity 45.2%; Pred. No. 1.4e-08; Matches 47; Conservative 16; Mismatches 33;
                                                                                                                                  InterPro; IPR001806; ...
InterPro; IPR001801; ...
Pfam; PF000081; EGF; 2.
Pfam; PF004031; CUB; 5.
Pfam; PF00400; Astacin; 1.
PRINTS; PR00400; ASTACIN.
PROSITE; PS00100; ASX_HYDROXYL; 2.
PROSITE; PS01180; CUB; 5.
PROSITE; PS01180; EGF_C2; 2.
PROSITE; PS01187; EGF_CA; 2.
PROSITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFam; PF0008; EGF; 1.
Pfam; PF00431; CUB; 3.
Pfam; PF01401; ASTACIN; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS01180; CUB; 3.
PROSITE; PS01180; EGF 2; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus laevis (African clawed frog).
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InterPro; IPR000130; ...
InterPro; IPR000152; -.
InterPro; IPR000561; -.
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                                                                                                                InterPro; IPR000859; -
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NCBL_TaxID=8355;
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SMART; SM00042; CUB; 1
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595 LSPDAKLHGRFCGSET-PEVITSQSNNMRVEFKSDNTV-SKRGFRAHF 640
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Q9Y6L7
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Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
Mrediction of the coding sequences of unidentified human genes. XIII.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
DNA Res. 6:63-70(1999).
HSSP; P00736; 1APQ.
Calcium-binding; EGF-11ke domain; Glycoprotein; Hydroxylation; Repeat. SEQUENCE 735 AA; 83575 MW; 45B29C813F79DBE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00042; CUB; 1.
Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
                                                                                                                                                                         NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human),
bustaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                               8;
                                                                                     Length 735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 10.0%; Score 185; DB 4; Length 926; I Similarity 45.4%; Pred. No. 4.4e-08; 49; Conservative 14; Mismatches 37; Indels
                                                                                                                               34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58FA35CDDE10970B CRC64;
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                                                                                                                                                                                                                                                                                   645 LTSDSKLHGKFCGT-ELPAVITSQYNNMRIEFKSDNTV-SKKGF 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                   10.1%; Score 186; DB 13;
45.2%; Pred. No. 2.6e-08;
ive 15; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                              926 AA
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PROSITE; PS00010; ASX_HYDROXYL; 2.
PROSITE; PS01180; CUB; 5.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 2.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99246063; PubMed=10231032;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KIAA0932 PROTEIN (FRAGMENT)
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                                                                  Ouery Match
Best Local Similarity 45.2%
                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000130; -. InterPro; IPR000152; -.
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InterPro; IPR000859; -
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Best Local Similarity
Matches 49; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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SEQUENCE
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Q9UQ00;
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09U000
0C 09U000
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Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat. SEQUENCE 1015 AA; 113556 MW; 25F5B23065861593 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                       Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                      Scott I.C., Greenspan D.S.;
"Sequence of the human mammalian tolloid-like 2 (n
chromosomal localisation of the cognate gene TLL2
Dev. Biol. 0:0-0(1999).
EMBL; RAF05916; AAD42979.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0480; ASTACIN, PROSITE; PSO0010; ASX_HYDROXYL; 2. PROSITE; PS01180; CUB; 5. PROSITE; PS01181; EGF_2; 2. PROSITE; PS01187; EGF_CA; 2. PROSITE; PS01187; EGF_CA; 2. PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1. SMART; SM00042; CUB; 1.
PRT; 1015
                                               Created)
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                                     01-00-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-NOX-2001 (TrEMBLrel. 16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00431; CUB; 5.
Pfam; PF01400; Astacin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
PRELIMINARY;
                                                                     01-NOV-1999 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
TOLLOID-LIKE 2 PROTEIN.
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Interpro; IPR000859; -
Interpro; IPR001506; -
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Best Local Similarity
Matches 49; Conservat
                                                                                                                                                                               (Human)
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                               Homo sapiens
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PRINTS; PR00480; ASTACIN.
PROSITE; PS00010; ASTALYDROXYL; 2.
PROSITE; PS01180; CUB; 5.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 2.
PROSITE; PS01042; ZIUC_PROTEASE; UNKNOWN_1.
SMART; SM00042; CUB; 1.
Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
SEQUENCE 1012 AA; 113252 MW; 72EEE268A4D8C5FE CRC64;
Thomas C.L., Scott I.C., Maas S.A., Clark T.G., Greenspan D.S.;
"Sequence of murine mammalian tolloid-like-2 (mTl1-2) and chromosomal localization of the cognate gene Tl12.";
Docalization 0:0-0(1999)
EMBL, AF073526; AAD42993.1;
HSSP; P00742; 1HCG.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Hirahara I., Tomita M., Umeyama K., Urakami K.;
Hirahara I., Tomita M., Umeyama K., Urakami K.;
"New splicing pattern of the gene for procollagen C-proteinase.";
Cell Struct. Funct. 23:125-125(1998).
EMBL; AB012139; BAA75639.1; -.
HSSP; P00736; 1APQ.
MEROPS; M12.005; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
8
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9.9%; Score 183; DB 11; Length 1012;
Best Local Similarity 44.4%; Pred. No. 7.5e-08;
Matches 48; Conservative 15; Mismatches 37; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 681 LSPDAKLHGKFCGSET-PEVITSQSNNMRVEFKSDNTV-SKRGFRAHF 726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PROCOLLAGEN C-PROTEINASE 3 (FRAGMENT)
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R flaterPro; IPR001881; -.
R Pfam; PF00008; EGF; 1.
R PROSITE; PS00010; ASX_HYDROXYL; 1.
R PROSITE; PS01180; CUB; 2.
R PROSITE; PS01180; EGF_C3; 1.
R PROSITE; PS01186; EGF_C3; 1.
R PROSITE; PS01186; EGF_C3; 1.
R SMART; SM00042; CUB; 1.
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                                                                                                                                                                           MGD; MGI:1346044; TII.2.
InterPro; IPR000130; -.
InterPro; IPR000152; -.
InterPro; IPR000551; -.
InterPro; IPR00150; -.
INTERPRO; IPR0015
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SEQUENCE FROM N.A.
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Gilbertson DG; Sheppard PO, 03-MAY-1999; 99US-0304216. 10-NOV-1999; 99US-0164463. 04-FEB-2000; 2000US-0180169. 03-MAY-2000; 2000WO-US40047 (ZYMO ) ZYMOGENETICS INC. Gilbert T, Hart CE, WPI; 2000-687541/67 09-NOV-2000 

Murine vascular en A murine platelet-Murine TANGO 128. Human VEGF-X prote Human VEGF-X Prote Human VEGF-X prote Human VEGF-X prote A fragment of plat Lung cancer associ

AAB48658 AAY96861 AAY84559 AAB10631 AAB10632 AAB10642 AAB10637 AAB10637 AAB10638 AAY84558 AAY84558

345 345 180 1113 1113 1149 227 227 318

Mouse zvegf3, SEQ

Query Match

Score

Result No. (first entry)

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26-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       c vegf4 or fragments thereof, particularly human zvegf4/human zvegf4 or fragments thereof, particularly human zvegf4/human zvegf4 or fragments thereof, particularly human zvegf4/human zvegf4 cucleic acids; the recombinant expression of human zvegf4 an antibody which binds to human zvegf4 are a method of activating a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a method of modulating the proliferation, differentiation, migration or metabolism of bone cells, comprising exposing bone cells genetic zvegf4-derived polypeptides; and a method of detecting a genetic zvegf4-derived polypeptides; and a method of detecting a genetic zvegf4-derived polypeptides; and a method of detecting a genetic zvegf4-derived polypeptides; and a method of detecting a genetic fragments may be used to stimulate tissue development or repair, or cellular differentiation or proliferation. They are particularly used for the treatment or repair of liver damage, and may also be used to modulate neurite growth (e.g., in the treatment of Alzheimer's disease or multiple sclerosis). Due to their osteogenic activity, they may also be used in the treatment of periodontal disease and fractures. They may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to the human growth factor homologue zvegf4 (AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member of the PDGF (platelet-derived growth factor)/YEGF (vascular endothelial growth factor) family. Zvegf4 has a growth factor domain (ABA88654) characterised by a PDGF cystine knot structure, and a CUB domain characterised by a PDGF cystine knot structure. Zvegf4 has PDGF-like activity, having mitogenic activity on fibroblasts, vascular smooth muscle cells and pericytes, and has also been shown to stimulate bone growth. The invention also relates to fusion proteins comprising human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used to enhance expansion and mobilisation of haematopoietic stem cells and endothelial precursor stem cells, which may be useful in the treatment of ischaemia, in wound healing, and in the modulation of the immune system. The present sequence represents mouse zvegf3.
                                                                                                                       factor homologs and the nucleic acids that encode them, useful
                                                                                                                                                                               e.g. for treating liver damage, ischemia, multiple sclerosis and Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 130-131; 143pp; English.
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N-PSDB; AAC81583.
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                                                                                                                                     GRWCGSGTVPGKQTSKGNHIRIREVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS 180
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                                              1 MLLIGLILLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS
                                                        LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
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DB 21; Length 345;

1 MLLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS 60

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nurine 2VEGF3 are claimed. The growth factors comprise a growth factor domain and a CUB domain (generic sequence motifs are shown in AAY96859 and AAY96860). The growth factor domain is characterized by an arrangement of cysteine residues and beta-strands that is characteristic of the "cysteine knot" structure of the platelet-derived growth factor (bGF) family. The CUB domain shows homology to CUB domains in neuropilins, human bone morphogenetic protein-1, porcine seminal plasma crotein, bovine acidic seminal fluid protein and Xenopus laevis tolloid-like protein. Structural analysis and homology predict that zVEGF3 polypeptides complex with a second polypeptide to form multimeric proteins. The human zvegf3 gene has been mapped to chromosome 4q28 3.

ZVEGF3 polypeptides complex with a second polypeptide to form multimeric proteins. The human zvegf3 gene has been mapped to chromosome 4q28 3.

ZVEGF3 is useful for stimulating the growth of fibroblasts or smooth muscles cells, for activating cell surface PDGF-alpha receptor and for inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is useful for regulating (post-development) organ growth, regeneration and maintenance as well as tissue maintenance and repair processes. ZVEGF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel zveqf3 polypeptides and nucleotides encoding them useful for stimulating growth of smooth muscle cells and fibroblasts comprising an epitope bearing portion of a specific amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease, myocardial ischemia, vascular intimal hyperplasia, atherosclerosis, wound healing, chronic liver disease and heamangioma atherosclerosis, wound shealing, chronic liver disease and heamangioma formation. ZVEGF3 can also be used to modulate neurite growth and development of the nervous system, and for treating neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This shows a murine ZVEGF3 a novel vascular endothelial growth factor
                                                                                                                         Vascular endothelial growth factor; homologue; zvegf3; CUB domain;
                                                                                                                                           Cysteine knot; platelet derived growth factor; PDGF; neuropilin, chromosome 4q28.3; cytostatic; anti-psoriatic; anti-inflammatory; anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antagonists are useful for treating cancer, rheumatoid arthritis, diabetic retinopathy, ischemic limb disease, peripheral vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shoemaker KE;
                                                                             Murine vascular endothelial growth factor homologue, ZVEGF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 169-170; 173pp; English.
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N-PSDB; AAA51527.
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21-OCT-1999;
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                                                                                                                                                                                                                  vulnerary
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and/or growth or motility of cells expressing a PDGF-C receptor.

PDGF-C polypeptides can be used in pharmaceuticals for promoting cell
proliferation, preferably in combination with one other growth factor
and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also
be used for stimulating connective tissue or wound healing. The
PDGF-C polypeptide can be enzymatically processed to generate the active
truncated form of PDGF-C and used to regulate the receptor-binding
specificity of PDGF-C. PDGF-C can also be used to promote fibroblast
mitogenesis in a mammal and to induce PDGF alpha receptor activation.
PDGF-C antagonists can be used to inhibit tumour growth of a tumour
CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.
choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
and erythroleukemia, can be identified by testing for expression of
PDGF-C. PDGF-C antagonists can also be used to inhibit tissue
remodelling during invasion of tumour cells into a normal population of
cells, Antagonists can also be used to inhibit conditions,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation, differentiation, growth and motility of cells expressing the PDGF-C \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Platelet-derived growth factor C; PDGF-C; cell proliferation; growth factor; heparin; connective tissue; wound healing; VBGF-F; fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth; choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia; lung carcinoma; erythroleukemia; tissue remodelling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents murine platelet-derived growth factor (PDGF-C) (formally designated VEGF-F). PDGF-C polypeptides have the ability to stimulate and enhance proliferation or differentiation,
                                                           PKFPHTYPRNMYLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL
                                                                                              GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS
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                                                                                                                                                                                                                                                                         murine platelet-derived growth factor C (PDGF-C).
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Betsholz C;
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Heldin C,
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21-MAY-1999;
15-JUL-1999;
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                                            Gaps
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systemic lupus erythematosus; transgenic animal; diagnosis;
                                                                                                         1 MILLGLILLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS 60
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inflammatory bowel disease; septic shock; ulocrative collitis;
Crohn's disease; chronic myelogenous leukemia; cancer; liver
disease; Hodgkin's disease; osteoarthritis; Lyme's disease;
  Length 345;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prophylatic; therapeutic; mouse.
Score 345;
Pred. No. 0;
                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB01427 standard; Protein; 180 AA.
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0
  100.0%;
                   100.08;
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                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Misc-difference 129
                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine TANGO 128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-OCT-2000
                                            345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prognosis;
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Gosiewska A;

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This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has valinaray, cytostatic, antirheumatic, antirheumatic, antirheumatic, antirheumatic, antirheumatic, antirheumatic, antiporiatic and ridiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair psy promoting angiogenic activity or vascularization. This sequence repairs the human VEGF-X protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiathritic; antipsoriatic; antidabetic; tradiment; anglogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
    rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 LYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP
                                                                                                                                                                                                                                                                                                                                                                                                                                      Yon JR, Dijkmans JJH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21; L
5.9e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.1%; Score 52; DB 100.0%; Pred. No. 5.9 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB10632 standard; Protein; 113 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1; 127pp; English.
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                                                                                                                                                                                                                                                                                          98GB-0028377.
                                                                                                                                                                                                                                              99WO-US30503
                                                                                                                                                                                                                                                                                                                                         99US-0164131
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sprengel JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                       (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-442669/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
Les 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAA71936
                                                                                                                                                WO200037641-A2
                                                                                                                                                                                                                                                                                        22-DEC-1998;
18-MAR-1999;
08-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SN,
                                                                                                    Homo sapiens
                                                                                                                                                                                                                                           21-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JAN-2001
                                                                                                                                                                                               29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gordon RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dhanaraj
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, postriasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chiseases e.g. myasthemia gravis, autoimmune diseases e.g. myasthemia gravis, autoimmune disbetes and systemic clupus erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in forensic biology, for diagnostic assays, prognostic assays, copnostic assays, prognomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a disorder associated with aberrant TANGO expression. A wide range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 180;
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    "Unidentified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arthritis, psoriasis and autoimmune diseases
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                                                   "Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cellular disorders can be treated
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                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                          98US-0223546.
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Best Local Similarity 100.
Matches 94; Conservative
/note=
Misc-difference 167
                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-465743/40.
                                                                         Misc-difference 172
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                                                                                                                                              WO200039284-A1
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Sequence

16

à g ò

92

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Gaps

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Length 113;

99

AAB10631;

AAB10631

RESULT

Yon JR, Dijkmans JJH, Gosiewska A;

Sprengel JJ,

Xu J;

98GB-0028377. 99US-0124967. 99US-0164131.

99WO-US30503

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(JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-442669/38
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                                                        WO200037641-A2.
                                                                                                                                                                                                                                                                                                                 Chanaraj SN,
                      Homo sapiens
                                                                                                                                  21-DEC-1999;
                                                                                                                                                                                            18-MAR-1999;
08-NOV-1999;
                                                                                                                                                                          22-DEC-1998;
                                                                                              29-JUN-2000
                                                                                                                                                                                                                                                                                            Gordon RD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, extostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the human VEGF-X protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                                                                                                                                                                                                                                                                                                               New vascular endothelial growth factor protein, useful for treating or
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5.9e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.1%; Score 52; DB 100.0%; Pred. No. 5.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB10642 standard; Protein; 149 AA
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                                                                                                                                                                                                                                  99US-0124967.
99US-0164131.
                                                                                                                                                                            99WO-US30503
                                                                                                                                                                                                                98GB-0028377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                            (JANC ) JANSSEN PHARM NV.
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-442669/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 AA;
                                                                                                WO200037641-A2
                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                     Dhanaraj SN,
                                                                                                                                                                            21-DEC-1999;
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08-NOV-1999;
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                                                                                                                                                                                                                  22-DEC-1998;
                                                                                                                                      29-JUN-2000
                                                                                                                                                                                                                                                                                                                                   Gordon RD,
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VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 15.1%; Score 52; DB 21; 1
100.0%; Pred. No. 7.4e-42;
iive 0; Mismatches 0;
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                                                                  Disclosure; Fig 24; 127pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human VEGF-X protein #2.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       149 AA;
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Yon JR, Dijkmans JJH, Gosiewska A;

Sprengel JJ,

Xu J;

99US-0124967. 99US-0164131.

99WO-US30503 98GB-0028377

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New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 18; 127pp; English.
                                                                                                                                                                    (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                         WPI; 2000-442669/38
                                                                                                                                                                                                                                                       N-PSDB; AAA71982
                             WO200037641-A2
    Homo sapiens.
                                                                                                                                                                                                               Dhanaraj SN,
                                                                                   21-DEC-1999;
                                                                                                                22-DEC-1998;
                                                                                                                             18-MAR-1999;
08-NOV-1999;
                                                        29-JUN-2000
                                                                                                                                                                                                  Gordon RD,
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                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, gytostatic, antinhemmatic, antinhemical antipocriatic and antidabetic activity and acts as a nangiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating corp reventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote tissue regeneration and organ repair, proliferation of new blood vessels, tissue regeneration and organ repair, by promoting angiogenic activity or vascularization. This sequence represents a human VEGF-X protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEGE-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; anglogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                                                                                                                                                                                             preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                               New vascular endothelial growth factor protein, useful for treating
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                                                                                                                                                                                                                Gosiewska A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 LYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 227;
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nes 0; Indels
                                                                                                                                                                                                               Dijkmans JJH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.1%; Score 52; DB 100.0%; Pred. No. 1.1 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 17; 127pp; English.
                                                                                                                                                                                                             Sprengel JJ, Yon JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB10638 standard; Protein; 227 AA
                                                                                                                                       99US-0124967.
                                                                                                99WO-US30503
                                                                                                                           98GB-0028377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 100. S2; Conservative
                                                                                                                                                                                 (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human VEGF-X protein #3.
                                                                                                                                                                                                                                                     WPI; 2000-442669/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 AA;
                                                                                                                                                                                                                                                                     N-PSDB; AAA71981
                                        WO200037641-A2
                Homo sapiens.
                                                                                                                                                                                                                            Dhanaraj SN,
                                                                                                21-DEC-1999;
                                                                                                                          22-DEC-1998;
                                                                                                                                         18-MAR-1999;
                                                                                                                                                    08-NOV-1999;
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                                                                    29-JUN-2000
                                                                                                                                                                                                             Gordon RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Best Local (
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AAB10638
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This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, oylostatic, antinheumatic, antiarthritic, antipheumatic, antiarthritic, antipheumatic, antipheumatic, antipheumatic, antipheumatic, antipheumatic, antipheumatic, antipheumatic, antipheumatic, and vascularization and acts as an angiogenesis and vascularization crequiator. An antisense molecule of the invention is useful for treating cancer, rheumaticid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and itssue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence repersents a human VEGF-X protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Platelet-derived growth factor C; PDGF-C; cell proliferation; growth factor; heparin; connective tissue; wound healing; VBGF-F; fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth; choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia; lung carcinoma; erythroleukemia; tissue remodelling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 LYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.1%; Score 52; DB 21; Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A fragment of platelet-derived growth factor C (PDGF-C).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY84558 standard; Protein; 318 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Lung cancer associated polypeptide sequence SEQ ID 776.
                                                                                                                              WO200055180-A2
                                                                                                                                                                                                                              (HUMA-) HUMAN
                                                                                                         Homo sapiens
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                                                                                                                                                      21-SEP-2000
                                                                                                                                                                                                                                                                   Ruben SM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and/or growth or motility of cells expressing a POGF-C receptor.

DGF-C polypeptides can be used in pharmaceuticals for promoting cell
proliferation, preferably in combination with one other growth factor
and heparin. Pharmaceuticals comprising POGF-C polypeptides can also
be used for stimulating connective tissue or wound healing. The
POGF-C polypeptide can be enzymatically processed to generate the active
truncated form of POGF-C and used to regulate the receptor-binding
truncated form of POGF-C and used to regulate the receptor-binding
pecificity of POGF-C. POGF-C can also be used to promote fibroblast
mitogenesis in a mammal and to induce POGF alpha receptor activation.
POGF-C antagonists can be used to inhibit tumour growth of a tumour
corpressing POGF-C in a mammal. Specific types of human tumours, e.g.
choriocarcinoma, Wilms tumour, megakarryoblastic leukaemia, lung carcinoma
and erythnoleukemia, can be identified by testing for expression of
POGF-C. POGF-C antagonists can also be used to inhibit tissue
remodelling during invasion of tumour cells into a normal population of
cells. Antagonists can also be used to treat fibrotic conditions,
especially found in the lung, kidney or liver.
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                                                                                                                                                                                                                                                                                                                            Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation, differentiation, growth and motility of cells expressing the PDGF-C \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                       Alitalo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 318;
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                                                                                                                                                                                                                                                       Uutela M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             red. No. 1.4e-41;
Mismatches 0;
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Pred. No. 1.4e-41
                                                                                                                                                                                                                                                     Lee X, Ponten A,
Betsholz C;
                              /note= "encoded by AAS"
                                                                                                                                                                                                                 (LUDW-) LUDWIG INST CANCER RES. (UYHE-) UNIV HELSINKI LICENSING LTD.
Location/Qualifiers
287
                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 4; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.1%; Scc.
100.0%; Pre
0;
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                                                                                                                                          98US-01108109.
98US-0110749.
98US-0113002.
                                                                                                      99WO-US22668
                                                                                                                             98US-0102461
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Heldin C,
                                                                                                                                                                                                                                                                                         2000-292954/25.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 AA;
                                                                                                                                                                                                                                                                                       WPI; 2000-292954,
N-PSDB; AAA12524
                 Misc-difference
                                                     WO200018212-A2
                                                                                                                                                    03-DEC-1998;
18-DEC-1998;
21-MAY-1999;
15-JUL-1999;
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                                                                                                    30-SEP-1999;
                                                                                                                                                                                                                                                 Eriksson U,
                                                                              06-APR-2000
                                                                                                                             30-SEP-1998
                                                                                                                                           12-NOV-1998
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ID AAB5
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AC AAB5
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DT 14-M
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                                                                                                           antibacterial; diagnosis; neural disorder; immune disorder; reproductive; proliferative disorder; wound healing; infectious disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antagonists may have neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal general; nephrotropic; antilinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                  cardioactive; immunomodulatory; muscular active; vulnerary; gastrointestinal; nephrotropic; antlinfective; gynecological;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 1305-1306; 1425pp; English.
cancer associated protein;
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100.0%; F1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                990S-0124270.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-587514/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       such as lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Watches 52; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ROSE/) ROSEN C A.
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AAY41766;

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This invention describes the isolation of a novel human vascular endothelial cell growth factor-E (VEGF-E) polypeptide which has cranquillizer, vulnery and cardiant activity. VEGF-E can be administered therapeutically, especially by expressing encoding polynucleotides, to treat cardiovascular or endothelial disorders in mammals, especially humans. It is useful in wound repair and tissue generation and regeneration, and may especially be used to treat cardiac hypertrophy it can be combined with a carrier in pharmaceutical compositions, which can be administered to treat disorders as above. VEGF E can be used to screen for antagonists, and aponists, and the antagonists administered to treat angiogenic disorders in mammals (especially humans) e.g. cancer or serul therapeutically as antagonists, as above. The antibodies are also useful to detect VEGF-E polypeptide, especially to diagnose cardiovascular, endothelial or angiogenic disorders in mammals (e.g. vascular disease, or neovascularization associated with tumor formation of an antibody vegef-E polypeptide complex. Polynucleotides encoding vegef-E can be used to diagnose cardiovascular and endothelial disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in mammals, by detecting abnormally high or low VEGF-E gene expression in tissue samples. They can also be used to diagnose a disease or susceptibility to a disease related to a mutated form of VEGF-E (e.g. a cardiovascular, endothelial or angiogenic disorder such as a tumor), by detecting a mutation in the VEGF-E-encoding sequence isolated from a
                    treatment; cardiovascular disorder; endotĥelial disorder; therapy; tissue generation; regeneration; cardiac hypertrophy; cancer; detection; angiogenic disorder; age-related macular degeneration; vascular disease; neovascularization; tumor; gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sample. They may also be used to produce probes useful to detect related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene mapping. This sequence represents the human VEGF-E in the method of the invention.
VEGF-E; human; vascular endothelial cell growth factor; wound repair; treatment; cardiovascular disorder; endothelial disorder; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New growth factor polypeptide useful for treating cardiovascular or endothelial disorders, e.g. cardiac hypertrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 2; 122pp; English.
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                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
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                                                                                                                                    Homo sapiens
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15.1%; Score 52; DB 20; Length 345; 100.0%; Pred. No. 1.5e-41; ive 0; Mismatches 0; Indels
                      Best Local Similarity 100.
Matches 52; Conservative
Query Match
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Gaps

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247 LYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP 298

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AAY41766 standard; Protein; 345 AA
RESULT 13
         AAY41766
ID AAY4
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Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein.
                           Human PRO200 protein sequence.
                                                                                                                                                                                                                                         98US-0079689.
98US-0079728.
                                                                                                                99WO-US05028
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98US-0080194
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             (first entry)
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                                                                                    W09946281-A2.
                                                                       Homo sapiens
             07-DEC-1999
                                                                                                                08-MAR-1999;
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growth factor related protein; VEGF-R protein;

Vascular endothelial

Human vascular endothelial growth factor related protein.

(first entry)

11-0CT-1999

AAY30023;

standard; Protein; 345 AA.

tissue growth inhibition; tumour growth; cancer; tissue growth; anglogenesis; coronary artery blockage.

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The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AA234891 to AA234338, and AA141685 to AA41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular
                                                                                                                                                                                                                                                                                                                                                                                                                Chen J;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Baker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Fig 207; 530pp; English.
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                              98US-0084411.
98US-0084411.
98US-0084600.
98US-0084627.
98US-0084637.
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980S-0085338
980S-0085339
980S-0085573.
980S-0085579.
980S-0085580.
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980S-0085697.
980S-0085700.
980S-0085704.
980S-0086392.
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98US-0086486.
98US-0087098.
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98US-0094651
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98US-0084
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                              06-MAY-1998;
06-MAY-1998;
07-MAY-1998;
07-MAY-1998;
07-MAY-1998;
07-MAY-1998;
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A vascular endothelial growth factor related protein and related polynucleotide, useful for identifying antagonists and binding

98US-0098548. 98US-0072635. 98US-0088089. 98US-0090544.

27-JAN-1998; 05-JUN-1998; 24-JUN-1998;

31-AUG-1998;

Song HY; & CO ELI.

Na S,

Dou S,

(ELIL ) LILLY

WPI; 1999-458680/38.

N-PSDB; AAX86352

99WO-US01574

26-JAN-1999;

WO9937671-A1 Homo sapiens

29-JUL-1999.

Claim 1; Page 56-58; 62pp; English.

compounds

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Human; zvegf3; zvegf4 fusion; growth factor homologue; VEGF/PDGF family;
CUB domain; PDGF-like activity; mitogenic; osteogenic;
neovascularisation; tissue repair; proliferation; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            related (VEGF-R) protein. VEGF-R can be used in assays to identify compounds that bind to it or that unragonize its activity. VEGF-R antiaponists (e.g. anti-VEGF-R antibodies) are useful for inhibiting tissue growth. This is useful for inhibiting tumour growth and for treating cancer. VEGF-R itself can be used to stimulate tissue growth, angiogenesis and to traat coronary artery blockage. The VEGF-R coding sequence can be used for the recombinant production of
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Best Local Similarity
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Matches
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Gaps

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Indels

Length 345;

147 lysctprnfsvsireelkrtdtifwpgcllvkrcggncacclhncnecqcvp 298

RESULT 14 AAY30023

247 LYSCIPRNESVSIREELKRIDIIFWPGCLLVKRCGGNCACCLHNCNECQCVP

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Query Match 15.1%; Score 52; DB 20; L Best Local Similarity 100.0%; Pred. No. 1.5e-41; Matches 52; Conservative 0; Mismatches 0;

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nucleic acids; the recombinant expression of human zvegf4; an antibody which binds to human zvegf4 or a fragment thereof; a method of activating a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a method of modulating the proliferation, differentiation, migration or metabolism of bone cells, comprising exposing bone cells to zvegf4-derived polypeptides; and a method of detecting a genetic abnormality in the zvegf4 gene of a patient. Zvegf4 proteins and derived abnormality in the zvegf4 gene of a patient. Zvegf4 proteins and derived cellular differentiation or proliferation. They are particularly used for the treatment or repair of liver damage, and may also be used to modulate neurite growth (e.g., in the treatment of Alzheimer's disease or multiple sclerosis). Due to their osteogenic activity, they may also be used in the treatment of periodontal disease and fractures. They may also be used to net the activity and mobilisation of haematopoietic stem cells and endothelial precursor stem cells, which may be useful in the treatment of ischaemia, in wound healing, and in the modulation of the immune system. The present sequence represents human zvegf3.
liver damage; neuroregenerative; Alzheimer's disease; multiple sclerosis; periodontal disease; bone fracture; wound healing; vulnerary; ischaemia; immunomodulation; hepatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4.is a member of the PDGF (platelet-derived growth factor)/VBGF (vascular endothelial growth factor) family. Zvegf4 has a growth factor domain (AAB48654) characterised by a PDGF cystine knot structure, and a CUB domain (AAB48655) which has a beta barrel structure. Zvegf4 has PDGF-like activity, having mitogenic activity on fibroblasts, vascular smooth muscle cells and pericytes, and has also been shown to stimulate bone growth. The invention also relates to fusion proteins comprising human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Growth factor homologs and the nucleic acids that encode them, useful e.g. for treating liver damage, ischemia, multiple sclerosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zvegf4 or fragments thereof, particularly human zvegf4/human zvegf3
fusions; expression constructs and host cells comprising human zvegf4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the human growth factor homologue zvegf4
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sheppard PO, Gilbertson DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 48; Page 125-126; 143pp; English.
                                                                                                                                                                                                                                                                                       03-MAY-1999; 99US-0304216.
10-NOV-1999; 99US-0164463.
04-FEB-2000; 2000US-0180169.
                                                                                                                                                                                                                                          03-MAY-2000; 2000WO-US40047
                                                                                                                                                                                                                                                                                                                                                                                       (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gilbert T, Hart CE,
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Alzheimer's disease -
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                                                                                                                                            WO200066736-A1
                                                                                                Homo sapiens
                                                                                                                                                                                           09-NOV-2000
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Query Match 15.1%; Score 52; DB 21; Length 345; Best Local Similarity 100.0%; Pred. No. 1.5e-41; Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

247 LYSCTPRNESVSIREELKRIDTIEWPGCLLVKRCGGNCACCLHNCNECQCVP 298

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Db 247 lysctprnfsvsireelkrtdtifwpgcllvkrcggncacclhncnecqcvp 298

Search completed: September 5, 2001, 10:56:31 Job time: 113 sec

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APPLICANT: Del Vecchio, Alfred
TITLE OF INVENTION: HEPATITIS C VIRUS NS5B TRUNCATED PROTEIN
TITLE OF INVENTION: HEPATITIS C VIRUS NS5B TRUNCATED PROTEIN
TITLE OF INVENTION: AND METHODS THEREOF TO IDENTIFY ANTIVIRAL COMPOUNDS
FILE REFERENCE: P50743
CURRENT APPLICATION NUMBER: US/09/208,140
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
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Patent No. 6228576
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APPLICANT: Del 1904
TITLE OF INVENTION: HEPATITIS C VIRUS NS5B TRUNCATED PROTEIN
TITLE OF INVENTION: HEPATITIS C VIRUS NS5B TRUNCATED PROTEIN
FILE REFERENCE: P50743
CURRENT APPLICATION NUMBER: US/09/208,140
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NOS: 34
SOFTWARE: PASTSEQ for Windows Version 3.0
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                                              US-07-690-192-2
US-08-487-550-2
US-08-812-586-16
US-08-487-550-10
US-08-487-550-6
US-08-487-550-6
US-08-078-311-14
US-08-078-311-24
US-08-460-402-14
US-08-460-402-14
US-08-460-402-24
US-08-408-969-17
US-08-092-270-2
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. 1.8;
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100.0%; Pred. No.
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100.0%; Pic
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Best_Local Similarity
Matches 8; Conserv
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; ORGANISM: Viral
US-09-208-140-5
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; ORGANISM: Viral
US-09-208-140-6
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(without alignments)
576.129 Million cell updates/sec
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Patent No. 5338678
Patent No. 5338678
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Sequence 4, A
Sequence 12,
Sequence 14,
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Sequence 3,
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.. /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-572-225-1
US-08-938-365-3
US-08-749-169A-3
US-08-130-032A-3
US-08-07-925-695-5
US-08-957-001B-22
US-08-957-001B-22
US-08-957-001B-22
US-08-957-001B-22
US-08-957-001B-22
US-08-957-001B-22
US-08-957-01B-22
US-08-957-01B-22
US-08-957-01B-22
US-08-957-01B-2
US-08-096-762-185
US-08-096-762-185
US-08-096-762-185
US-08-096-762-185
US-08-468-671-14
US-08-468-671-14
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US-08-460-402-4
US-08-855-825-12
US-08-855-825-14.
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                                                                                                                                                                                                                                                                                                                US-09-457-066-43
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seq length: 200000000
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Match Length
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Maximum DB :
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Meiklejohn, Ph.D., Anita L.
                 ADDRESSEE:
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Matches
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                                Gaps
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                                                                                                                                                                                                                                                            APPLICANT: LI, Shi-Wu
APPLICANT: Sieron, Aleksander
APPLICANT: Brenner, Mitch
TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND ITS USE FOR
TITLE OF INVENTION: DRUG DEVELOPMENT FOR THE TREATMENT OF DISEASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 788;
                                0; Indels
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APPLICATION NUMBER: US/08/572,225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Yang, Pan
TITLE OF INVENTION: HUCHORDIN AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.3%; Score 8; DB 1;
100.0%; Pred. No. 19;
ive 0; Mismatches
               Pred. No. 1.8;
                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8389-031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
100.0%; Pre
                                                                                                                                                                             Sequence 1, Application US/08572225
Patent No. 5807981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08938365
Patent No. 5989909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFRENCE/CDOCKET NUMBER: 8386
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
                                                                                                                                                                                                                             Prockop, Darwin J.
Hojima, Yoshio
Li, Shi-Wu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 788 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 788 amino acids TYPE: amino acid
             Best Local Similarity 100.
Matches 8; Conservative
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1:
CLASSIFICATION:
                                                                                30 LLLGLLLL 37
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US-08-938-365-3
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                                                                                                                                                            US-08-572-225-1
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APPLICANT: Yang, Pan
TITLE OF INVENTION: HUCHORDIN AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 255 Franklin Street
CITY: Boston
                                                                                                                               MEDLUM LIFE. CALCOLOGICAL COMPUTER: DATE: WINDOWS 95
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,365
FILING DATE: 26-SEP-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: 1BM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastEEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTOKNEY/AGNOVENEY/AGNOV:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 2, Application US/08938365
; Patent No. 5989909
                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 0940
TELECOMMUNICATION INFORMATION:
TELEFAX: 617/542-8906
TELEX: 200154
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 855 amino acids
amino acid
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                                                                                                                          Diskette
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              225 Franklin
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Diskett
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                                                                                      ZIP: 02110-2804
COMPUTER READABLE FORM:
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Fish
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nes 8; Conserv
                                                                                   02110-2804
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ZIP: 02110-2804
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                                     Boston
                                                                      USA
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                                                                                                                      MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                      COUNTRY:
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12 LLLGLLLL 19
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                                                                               US-09-130-032A-3
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US-07-925-695-5
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,169A
                                                                                                                                                                                                                                                                                                              2.3%; Score 8; DB 2
100.0%; Pred. No. 21;
Live 0; Mismatches
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/040001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8006
TELER: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 867 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: RACIE, Lisa
APPLICANT: LAYALLIE, Edward
APPLICANT: DEROBERIES, Edward
TITLE OF INVENTION: CHORDIN COMPOSITIONS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BE PC compatible
OOPPRTER: PE PC CODS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08749169A Patent No. 5846770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R.
REGISTRATION NUMBER: 32,618
REFERRICE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (617) 498-8260
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 amino acids
                                                                                                                                                                                                                                                                                                                Query Match 2.3'
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-938-365-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-749-169A-3
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US-08-749-169A-3
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Sequence 5, Application US/07925695
Patent No. 5428145
GENERAL INFORMATION:
APPLICANT: OKAMOTO, Hiroaki
APPLICANT: OKAMOTO, Hiroaki
APPLICANT: NAKAWURA, NON-B HEPATITIS VIRUS GENOME,
TITLE OF INVENTION: POLYNUGLEDINES, POLYPEPTIDES, ANTIGEN, ANTIBODY AND
TITLE OF INVENTION: DETECTION SYSTEMS
NUMBER OF SEQUENCES:
OCHRESPONDENCE ADDRESS:
ADDRESSEE: Beveridge, Degrandi, Weilacher & Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Beveridge, DeGrandi, Weilacher & Young STREET: 1850 M Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,032A
FILING DATE: August 4, 1998
CLASSIFICATION: 530
                                                                 APPLICANT: LaVallie, Edward
APPLICANT: Racie, Lisa
APPLICANT: Recie, Lisa
APPLICANT: DeRobertis, Edward
TITLE OF INVENTION: HUMAN CHORDIN COMPOSITIONS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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100.0%; Pred. No. -.
0; Mismatches
                                                                                                                                                                                                             ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 3, Application US/09130032A Patent No. 5986056 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: LAZAR, Steven R.
REGIESTRATION UNDHER: 32,618
REFERENCE/DOCKET NUMBER: GI 52
RELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 848-8260
TELEFAX: (617) 846-881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 annino acids
TVPE: amino acids
TVPE: amino acids
TVPE: amino acids
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Best Local Similarity 100.،
اندم 8; Conservative
                                                                                                                                                                                                                                                                                   STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20036
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
                                                                                                                                                                                                                                                        CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: D. COUNTRY:
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Length 954; 0; Indels

Query Match 2.3%; Score 8; DB 2; Best Local Similarity 100.0%; Pred. No. 22; Matches 8; Conservative 0; Mismatches

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TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of TITLE OF INVENTION: Myeloproliferative Disease
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Merchant & Gould
90 South 7th Street, 3100 No. 5989833west Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,402
                                                                                                                                                                                                                                                                                                                                                                       Score 7; DB 2;
Pred. No. 7.4;
; Mismatches
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR90/00762
FILING DATE: 19-0CT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Kowalchyk, Katherine M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 8076.84USWO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUBER: WO PCT/FR90/00762
FILING DATE: 14-0CT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Charon, Martine
Gisselbrecht, Silvie
Penciolelli, Jean-Francios
Souyri, Michele
Tambourin, Pierre
Varlet, Paule
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                                                                                                                                                                                                                                                                                                                                                                             100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wendling, Francoise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
                                                                                                                                                           TELEPHONE: 612-332-530
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.0
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                         TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-078-311-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 436
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minneapolis
                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 LLGLLLL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 LLGLLLL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
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COUNTRY:
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APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-460-402-9
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VENTION: Polypeptide of a Growth Factor Receptor
VENTION: Family, Application in the Diagnosis and Treatment of
VENTION: Myeloproliferative Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/078,311
FILING DATE: 18-JUN-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Charon, Martine
Gisselbrecht, Silvie
Penciolelli, Jean-Francios
Souyri, Michele
Tambourin, Pierre
Varlet, Paule
                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/925,695
FILING DATE: 19920807
CLASSIFICATION: 435
PRIOR APPLICATION ATA:
APPLICATION NUMBER: JP 287402/91
FILING DATE: 09-A0G-1991
PRIOR APPLICATION NUMBER: JP 360441/91
FILING DATE: 05-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Weilacher, Robert G.
REGISTRATION NUMBER: 06/87-480
TELECOMMUNICATION INFORMATION:
TELEPRONE: (202) 659-1462
TELEX: WUI 64470
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARATICS:
LENGTH: 3033 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5925750west Center
CITY: Minneapolis
   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.3
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Variet, Paule APPLICANT: Variet, Paule APPLICANT: Vigon, Isabel APPLICANT: Wendling, Era TITLE OF INVENTION: Fami TITLE OF INVENTION: Fami NUMBER OF SEQUENCES: 34 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Charon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3014 LLLGLLLL 3021
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US-07-925-695-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-078-311-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT
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Gaps ö

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Gaps
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STREET: One Liberty Place, 46th floor
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                                                                                                                                                                                                         APPLICANT: Williams, William V.
APPLICANT: Madaio, Michael
APPLICANT: Weiner, David B.
TITLE OF INVENTION: IMPROVED VACCINES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JABER: US 60/029,592
23-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/496,301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/957,001
FILING DATE: 23-0CT-1997
APPLICATION NUMBER: US 60/029,595
FILING DATE: 23-0CT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/08341219
Patent No. 5643877
GENERAL INFORMATION:
APPLICANT: ZODAT, Y.
                                                                                                                                                     ; Sequence 22, Application US/09496301; Patent No. 6248565; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: UF TELECOMMUNICATION INFORMATION TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.0
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 215 CT TELEPHONE: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-09-496-301-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                        STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gothilf, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                        LIGELEL 15
                    LIGITIT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                             19103
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                 US-09-496-301-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Woodcock Washburn Kurtz Mackiewicz & No. 6228621ris
One Liberty Place, 46th floor
                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                                                        Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 24;
                                                                                                                                                                                                                                                                                      Query Match 2.0%; Score 7; DB 2 Best Local Similarity 100.0%; Pred. No. 7.4 Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.0%; Score 7; DB 4
100.0%; Pred. No. 8.6
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,001B
FILING DATE: 23-OCT-1997
CLASSIFICATION: 424
PRIOR APPLICATION WASR: 05 60/029,592
FILING DATE: 23-OCT-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-3303
TELECOMUNICATION INFORMATION:
TELECHONE: 215-568-3109
                                        8076.840503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Williams, William V.
APPLICANT: Madaio, Michael
APPLICANT: Weiner, David B.
TITLE OF INVENTION: IMPROVED VACCINES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/08957001B Patent No. 6228621
                REGISTRATION NUMBER: 31,838
REPRENCE/POCKET UNMBER: 807
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: windows
NAME: Randall A. Hillson
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.03
Best Local Similarity 100.0
Matches 7; Conservative
                                                                                          TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Philadelphia
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-460-402-9
                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                          3 LLGLLLL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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US-08-957-001B-22
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Sequence 185, Application US/08053131
Patent No. 5661016
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Townsend and Townsend Khourie and Crew One Market Plaza, Steuart Tower, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IND PC compatible
SOFTWARE: Patently NG-DS/MS-DOS
SOFTWARE: Patently NG-DS/MS-DOS
SOFTWARE: Patently NG-DS/MS-DOS
CURRENT APPLICATION NUMBER: US/08/053,131
FILING DATE: 16-DEC-1992
PRIOR APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION NUMBER: US 07/853,408
APPLICATION NUMBER: US 07/853,408
APPLICATION NUMBER: US 07/853,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. ...
                                                                                                                                                     NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 3074
REFERENCE/DOCKET NUMBER: 8399-003-999
TELECOMNUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.0%; Score 7;
US/08/912,314A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 14643-9-3
                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/341,219
FILING DATE: 05-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Smith, William M. REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                  not relevant
                  30-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 18-MAR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                       LENGTH: 85 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 197 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.0
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              San Francisco
California
  APPLICATION NUMBER:
FILING DATE: 30-JUN
                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                           TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ANTI-SENSE: NO US-08-912-314A-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-053-131-185
                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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APPLICANT: Rivier, J.
APPLICANT: Rivier, J.
APPLICANT: Powell, J.
APPLICANT: Germood, N.
APPLICANT: Gethilf, Y.
TITLE OF INVENTION: Compounds and Methods For Controlling TITLE OF INVENTION: Reproduction in Fish
NUMBER OF SEQUENCES: Z.
CORRESPONDENCE ADDRESS:
  Compounds and Methods For Controlling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 85;
                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURREWY APPLICATION DATA:
APPLICATION NUMBER: US/08/341,219 FILING DATE: 05-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGNT INCRMATION:
NAME: COTUZZI,, LAURA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: COTUZZI, LAURA A.
REGISTRATION NUMBER: 30742
REFERENCE/DOCKET NUMBER: 8399-003-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 85 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                        Reproduction in Fish
                                      NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                          COUNTRY: USA
ZIP: 10036-2711
COMPUTER READBLE FORM:
MEDIUM TYPE BM PC compatible
OOMUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-912-314A-22
Sequence 22, Application US/08912314A
; Patent No. 6210927
; GENERAL INFORMATION:
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Best Local Similarity 100.0%; P.
Matches 7; Conservative 0;
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
TITLE OF INVENTION:
TITLE OF INVENTION:
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ZIP: 10036-2711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ANTI-SENSE:
US-08-341-219-22
                                                                                                                                 CITY: N
STATE:
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| TELECOMMUNICATION INFORMATION:
| TELEPHONE: 415-236-2400 |
| TELEPHONE: 415-326-2420 |
| TELEPHONE: 415-326-2420 |
| TELEPHONE: 415-326-2420 |
| INFORMATION FOR SEQ ID NO: 185: |
| SEQUENCE CHARACTERISTICS: |
| LENGTH: 116 amino acids |
| TYPE: amino acidd |
| TOPOLOGY: 1inear |
| MOLECULE TYPE: protein |
| JOS-08-053-131-185 |
| Ouery Match | 2.0%; Score 7; DB 1; Length 116; |
| Best Local Similarity 100.0%; Pred. No. 33; |
| Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps |
| Qy 3 LLGLLLL 9 |
| Db 9 LLGLLLL 15
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Search completed: September 5, 2001, 10:56:51 Job time: 113 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2001, 10:56:08 ; Search time 12.76 Seconds
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Run on: September 5, 2001, 10:56:08; Search time 12.76 Seconds (without alignments)
926.187 Million cell updates/sec
Title: US-09-457-066-43
Perfect score: 345
Sequence: 1 MLLGLLLTSALAGQRTGT......DVALEHHEECDCVCRGNAGG 345

Scoring table: OLIGO , Gapext 60.0

Gapop ou.u , Gapext ou.u Searched: 93435 seqs, 34255486 residues Word size : 0

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	P08686 homo sapien	P34033 cavia porce		Q28894 canis famil	P34735 pichia angu	canine	P98070 xenopus lae	P13497 homo sapien		Q60805 mus musculu	P57097 rattus norv	P32926 homo sapien		P37044 haplochromi	sparu	homo	homo	homo	homo	sacch	P40931 myeloprolif	P50415 ovis aries		P10154 oryctolagus		P26445 sus scrofa	P01374 homo sapien	Q44278 acinetobact	-	-	P52555 rattus norv		Q09816 schizosacch
SUMMARIES		ID	CPS1_HUMAN	CPBX_CAVPO	PLF4_RAT	EP4_CANFA	YLU2_PICAN	PEN3_ADECC	BMP1_XENLA	BMP1_HUMAN	BMP1_MOUSE	MERK_MOUSE	MERK_RAT	DSG3_HUMAN	POLG_HCVJ6	GON2_HAPBU	GON2_SPAAU	KV11_HUMAN	KV1J_HUMAN	KV1W_HUMAN	KV1X_HUMAN	FCY1_YEAST	MPL_MPLV	BCT7_SHEEP	SAP3_MOUSE	TNFB_RABIT	TNFB_BOVIN	TNFB_PIG	TNFB_HUMAN	GYRB_ACIS7	MTRA_METMA		ER29_RAT	- 1	YAC2_SCHPO
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Q12982 P56703 Q6327 Q61327 P17553 P21854 P4065 P4065	P16301 P04180 Q08758 P53761
NIP2_HUMAN WNT3_HUMAN WNT3_MOUSE CD72_HUMAN GYRB_ACIHA ISP7_SCHPO	LCAT_MOUSE LCAT_HUMAN LCAT_PAPAN LCAT_RABIT
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## ALIGNMENTS

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Genet. 91:236-240(1993).
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 HLA-linked steroid 21-hydroxylase
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Tusie-Luna M.-T., Lesser M., New M.I., White P.C.;
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hyperplasia due to 21-hydroxylase deficiency.";
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Amor M., Parker K.L., Globerman H., New M.I., White P.C.;
"Mutation in the CYP21B gene (Ile-172-->Asn) causes steroid 21-
                                                                                                                                             Tuale-Luna M.T., Speiser P.W., Dumic M., New M.I., White P.C.; "A mutation (Pro-30 to Leu) in CYP21 represents a potential nonclassic steroid 21-hydroxylase deficiency allele.";
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                                          Porter R.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93239181; PubMed-8478006; Medell A., Luthman H.; Redell A., Luthman H.; Riteroid 21-hydroxylase (P450c21); a new allele and spread mutations through the pseudogene.";
              CAH THR-268 AND SER-493
                                       Rodrigues N.R., Dunham I., Yu C.Y., Carroll M.C.,
                                                                                                                                                                                                                                                                      hydroxylase deficiency.";
Proc. Natl. Acad. Sci. U.S.A. 85:1600-1604(1988)
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                                                                                                                     VARIANT CAH LEU-30, AND VARIANT THR-268.
MEDLINE-91304433; Pubmed-2072928;
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MEDLINE=92039635; PubMed=1937474;
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                                                                                                                                                                                      Mol. Endocrinol. 5:685-692(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS CAH ASN-172 AND TRP-356
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                                                      Campbell R.D.;
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MEDLINE-97220598; PubMed-9067760;
Kitby-Keyyer L., Portter C.C., Donohoue P.A.;
#E380D: a novel point mutation of CYP21 in an HLA-homozygous patient
with salt-losing congenital adrenal hyperplasia due to 21-hydroxylase
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MEDLINE-98165791; PubMed-9497336;
Nikoshkov A., Lajic S., Vlamis-Gardikas A., Tranebjaerg L., Holst M., Wedell A., Luthman H.; Vlamis-Gardikas A., Tranebjaerg L., Holst M., Wedell A., Luthman H.; Courring mutants of human steroid 21-hydroxylase (P450c21) pinpoint residues important for enzyme activity and stability.";
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Hum. Mutat. 13:505-505(1999).
VARIANTS CAH ASN-172; ASN-236; LEU-281; PRO-483 AND SER-493.
MEDLINE=95268421; PubMed=7749410;
Barbat B., Bogyo A., Raux-Demay M.-C., Kuttenn F., Boue J.,
Simon-Bouy B., Serre J.-L., Boue A., Mornet E.;
"Screening of CYP21 gene mutations in 129 French patients affected steroid 21-hydroxylase deficiency.";
Hum. Mutat. 5:126-130(1995).
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MEDLINE-99335263; PubMed-10408778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98180883; PubMed=9580109; Ordonez Sanchez M.L., Ramirez Jimenez S., Lopez-Gutierrez A.U., Riba L., Gamboa-Gardiel S., Certillo-Hinojosa M., Altamirano-Bustamante N., Calzada-Leon R., Robles-Valdes C., Mendoza-Morfin F., Tusie-Luna M.T.; Molecular genetic analysis of patients carrying steroid 21-hydroxylase deficiency in the Mexican population: identification possible new mutations and high prevalence of apparent germ-line
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"A cluster of missense mutations at Arg356 of human steroid 21-
hydroxylase may impair redox partner interaction.";
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MEDLINE-99335271; PubMed=10408786;
Kapelari K., Ghanaati Z., Wollmann H., Ventz M., Ranke M.B.,
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Identification of CYP21 mutations, one novel,
conformational polymorphism (SSCP) analysis.";
Hum. Mutat. 13:172-172(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANTS CAH1 LEU-105 AND SER-453.
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VARIANT CAH ASP-380.
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MEDLINE=87144262; PubMed=3821732;
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Q28894;
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. THIS ISOZYME IS ACTIVE UPON P. NITROANISOLE, ANILINE, D-BENZPHETAMINE, DELTA(9).

FETRAHYDROCANNABINOL (THC) AND STRYCHNINE.

CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + OXIDIZED FLAVOPROTEIN + H(2).

SUBCELLULAR LOCATION: MEBRANE-BOUND. ENDOPLASMIC RETICULUM.

SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Purification of a cytochrome P450 isozyme belonging to a subfamily of P450 IIB from liver microsomes of guinea pigs."; Biochem. Biophys. Res. Commun. 172:607-613(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme; Microsome; Endoplasmic reticulum.
                                                                                                                                                                                                                                                                                      01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CYTCCHROME P450IIB (EC 1.14.14.1) (FRACMENT).
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-HARTLEY; TISSUE-Liver;
MEDLINE-91054472; PubMed-2173574;
Narimatsu S., Akutsu Y., Matsunaga T., Watanabe K., Yamamoto I.,
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0
                   Length 494;
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                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.3%; Score 8; DB 1; Length 20; 100.0%; Pred. No. 0.27; ive 0; Mismatches 0; Indels
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                                                            0;
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01-JAN-1988 (Rel. 06, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                   20 AA
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                 2.6%; Score 9; DB 1
100.0%; Pred. No. 0.4
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (Rel. 40, Last annotation PLATELET FACTOR 4 PRECURSOR (PF-4). SCYB4 OR PF4. Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE, AND CHARACTERIZATION.
               Query Match 2.6
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
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InterPro; IPR001128;
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                               CPBX_CAVPO
P34033;
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P06765;
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PLF4_RAT
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                                                                                                                                                                                                                                                                                                                                        Spectrometry...;
Eur. J. Biochem. 223:203-210(1994).

Eur. J. Biochem. 223:203-210(1994).

- FUNCTION: PLATELET FACTOR 4. NONCOVALENTLY BOUND TO A PROTEOGLYCAN MOLECULE. IS RELEASED DURING PLATELET AGGREGATION. PF4 NEUTRALIZES THE ANTICOAGULANT EFFECT OF HEPARIN BECAUSE IT BINDS MORE STRONGLY TO HEPARIN THAN TO THE CHONDROITIN-4-SULFATE CHAINS OF THE CARRIER MOLECULE. CHEMOTACTIC FOR NEUTRAPHILS AND MONOCYTES.

- SUBUNIT: HOMOTETRAMER.
- PROTEORY OF GAL-GALNAC DISACCHARIDE WHICH IS MODIFIED WITH SIALIC ACID RESIDUES (MACROHETEROGENEITY).

- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                       Ravanat C., Gachet C., Herbert J.-M., Schuhler S., Guillemot J.-C., Uzablaga F., Pleard C., Ferrara P., Freund M., Cascenave J.-F., Rat platelets contain glycosylated and non-glycosylated forms of platelet factor 4. Identification and characterization by mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
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15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR (CE4) (EPIDIDYMAL SECRETORY PROTEIN E4).
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00048; ILB; 1.
PRINTS; PR00437; SMALLCYTKCXC.
PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
Cytokine; Platelet; Proteoglycan; Heparin-binding; Chemotaxis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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Doi T., Greenberg S.M., Rosenberg R.D.;
"Structure of the rat platelet factor 4 gene: a marker for megakaryocyte differentiation.";
Mol. Cell. Biol. 7:898-904(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 105;
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BY SIMILARITY.
BY SIMILARITY.
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Pred. No. 1.2;
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                                                                                                                                                          O-GLYCOSYLATION.
MEDLINE=94307262; Pubmed=8033893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.3%; Sco.
100.0%; Pre
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87 B
31 O
11286 MW;
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InterPro; IPR001089; -.
InterPro; IPR001811; -.
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Best Local Similarity
Matches 8; Conserv
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373 AA;
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SEQUENCE 47
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Q65950;
                                                                                                                                                                                                                                                                    NON_TER
SEQUENCE
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PEN3_ADECC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-NRRL Y-5445;
MEDLINE-95028149; PubMed-7941737;
Agaphonov M.O., Poznyakovski A.I., Bogdanova A.I., Ter-Avanesyan M.D.;
"Isolation and characterization of the LEU2 gene of Hansenula
                                                                                                                                                                     Gaps
                                 TISSUE=Epididymis;
MEDLINE=95263175; PubMed=7744511;
Ellerbrock K., Pera I., Hartung S., Ivell R.;
"Gene expression in the dog epididymis: a model for human epididymal
function.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pichia angusta (Yeast) (Hansenula polymorpha).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL). 15AAF315BA13958C CRC64;
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01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL PROFEIN IN LEUZ 3'REGION (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 AA
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100.0%; Pre
0;
                                                                                                                         int. J. Androl. 17:314-323(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12951 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; S77395; AAB34264.1; -.
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Yeast 10:509-513(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal; Glycoprotein
                                                                                                                                                             TISSUE SPECIFICITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YLU2_PICAN
P34735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TUTZ_PICAN
ID XIUZ_PI
AC P34735,
DT 01-FEB
DT 01-FEB
DT 01-FEB
DT 01-FEB
OC SECHAN
OC SECHAN
OC SECHAN
OC NOSI-T
RN [1]
RN [1]
RN KA MEDLIN
RX MEDLIN
RA AGAPHO
RT POLYM
RT PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGNAL
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                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canine adenovirus type 1 (strain CLL), and Canine adenovirus type 1 (strain R1261). Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.NCBI_TaxID=69150, 69151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
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01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PENTON PROTEIN (VIRION COMPONENT III) (PENTON BASE PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                     38575 MW; 4E955FFF5D191750 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       477 AA; 53464 MW; B9FDF37407D0FDA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morrison M.D., Onions D.E., Nicolson L.; "Complete DNA sequence of canine adenovirus type 1."; J. Gen. Virol. 78:873-878(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.3%; Scor.
100.0%; Pred. No. 3...,
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     477 AA
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100.0%; Pred. No. 4.3
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          SER/THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 8; Db
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Pfam; PF01686; Adeno_Penton_B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97275900; PubMed=9129661;
                                                                                                                                                                                                                                             EMBL; U00889; AAA19110.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U55001; AAB05438.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAA69061.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.3
Best Local Similarity 100.
Matches 8; Conservative
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                     PIR; S43455; S43455.
InterPro; IPR002889; -.
Pfam; PF01822; WSC; 1.
Hypothetical protein.
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CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                  DISULFID
                     ACT_SITE
                                                        DISULFID
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           METAL
                                            METAL
                                                                                                                                                                                                                                                                                             BMP1_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00022; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; 1.
GROSITE; PS01187; EGF_CA; 1.
Growth factor; Cytokine; Repeat; Bone; Cartilage; Hydrolase; Protease; Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                         Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.;

"Cloning and expression of cDNA encoding Xenopus laevis bone morphogenetic protein-1 during early embryonic development.";

Gene 134:257-261(1993).

-!- FUNCTION: INVOLVED IN PATTERN FORMATION IN GASTRULA AND LATER DIFFRERENTATION OF DEVELOPING ORGANS.

-!- DEVELOPMENTAL STAGE: BLASTULA, ERRLY GASTRULA AND LATE GASTRULA.

-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

-!- SIMILARITY: CONTAINS 3 CUB DOMAINS.

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
                                                                                                                                                       Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                            01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-CT-2000 (Rel. 40, Last annotation update)
BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BONE MORPHOGENETIC PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METALLOPROTEASE
                                                                                       707 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS: PRO0480; ASTACIN.
PROSITE; PSO0142; ZINC_PROTEASE; 1.
PROSITE; PSO1180; CUB; 3.
                                                                                        PRT;
                                                                                                                                                                                                                                      TISSUE=Embryo;
MEDLINE=94085787; PubMed=8262384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L12249; AAA16313.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01400; Astacin; 1. Pfam; PF00431; CUB; 3. Pfam; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000130; ...
InterPro; IPR000152; ...
InterPro; IPR000561; ...
InterPro; IPR000569; ...
InterPro; IPR001506; ...
InterPro; IPR001801; ...
                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        707
284
397
509
551
                                                                                                                                                                                      Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1APO.
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                163 LDLLNNAV 170
           183 LDLLNNAV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; M12.005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein.
                                                                                      BMP1_XENLA P98070;
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                                                                  RESULT 7
BMP1_XENLA
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Janitz M., Heiser V., Boettcher U., Landt O., Lauster R.; "Three alternatively spliced variants of the gene coding for the human bone morphogenetic protein-1."; J. Mol. Med. 76:141-146(1998).
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"Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld)
are encoded by alternatively spliced transcripts which are
differentially expressed in some tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The C-proteinase that processes procollagens to fibrillar collagens is identical to the protein previously identified as bone morphogenic protein-1.";
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BMP1_HUMAN STANDARD; PRT; 986 AA. P1497; 013292; 099421; 099422; 099423; 014874; 01-487. 01-487. 01-487. 01-487. 01-590 (Rel. 13, Created) (1-5000 (Rel. 40, Last sequence update) (1-607-2000 (Rel. 40, Last annotation update) (1-607-2000 (Rel. 40, Last annotation update) (1-607-2000 (Rel. 40, Last annotation update) (PROPHOGENETIC PROPEIN 1 PRECURSOR (EC 3.4.24.19) (BMP-1) (PROCOLLAGEN C-PROTEINASE) (PCP) (MAMMALIAN TOLLOID PROTEIN) (MTLD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wozney J.M., Rosen V., Celeste A.J., Mitsock L.M., Whitters M.J., Kriz R.W., Hewlck R.M., Wang E.A.;
                                                                                                         BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                      ö
                         (CATALYTIC) (BY SIMILARITY)
                                                                                       SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li S.W., Sieron A.L., Fertala A., Hojima Y., Arnold W.V., Prockop D.J.;
                                                                                                                                                                                                                                                                                                                                                          Length 707;
                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS BMP1-4; BMP1-5 AND BMP1-6).
                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .) (Po
1B6980D716DC9B8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Novel regulators of bone formation: molecular clones activities.";
                                                                (BY (BY (BY )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 93:5127-5130(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 703-986 FROM N.A. (ISOFORM BMP1-3).
                                                                ZINC (CATALYTIC) ZINC (CATALYTIC)
                                                                                                                                                                                                                                                                                                                                                          DB 1;
5. 6.1;
                                                                                                                                                                                                                                                                                                                                                                        100.0%; Prea. ...
                                           BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                            Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM BMP1-1).
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                      ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=89072730; PubMed=3201241;
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                                                                                                                                                                                                                                                                                            80673 MW;
                                                                                                                                                                                                                                                                                                                                                            2.3%;
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Best Local Similarity الاست
احد 8; Conservative
6666
1176
1177
1180
1186
526
535
550
62
1105
326
562
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554
176
1170
1180
1186
514
521
537
62
105
532
532
547
707 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Placenta;
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DISULFID
                                                      DISULFID
                                                                           DISULFID
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CARBOHYD
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CONFLICT
CONFLICT
                                                                                                                                                                       VARSPLIC
VARSPLIC
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VARSPLIC
                         DISULFID
                                                                                                CARBOHYD
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                                                                                                                                           CARBOHYD
              DISULFID
                                                                                                                                                   VARSPLIC
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                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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              II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
                                           ALA-|-ASP IN TYPE I AND II PROCOLLAGENS AND AT ARG-|-ASP IN TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CUB 3.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
                                                                      ENZYME REGULATION: ACTIVITY IS INCREASED BY THE PROCOLLAGEN C-ENDYPE REGULATION: ACTIVITY IS INCREASED BY THE PROCOLLAGEN C-ENDOPEPTIDASE ENHANCER PROTEIN.

ALTERNATIVE PRODUCTS: 6 ISOFORMS; BMP1-1, BMP1-2, BMP1-3 (SHOWN HERE), BMP1-4, BMP1-5 AND BMP1-6; ARE PRODUCED BY ALTERNATIVE
Biol, Chem. 269:32572-32578(1994).
- FUNCTION: CLEAVES THE C-TERMINAL PROPEPTIDES OF PROCOLLAGEN I, AND II. INDUCES CARTILAGE AND BONE FORMATION.
- CATALYTIC ACTIVITY: CLEAVAGE OF THE C-TERMINAL PROPEPTIDE AT
                                                                                                                                                                                                                                                                                                                                                                                                                          R InterPro; IPR001805; ...
R InterPro; IPR001801; ...
R Pfam; PF01400; Astacin; 1.
R Pfam; PF00431; CUB; 5.
R Pfam; PF00008; EGF; 2.
R PRIMTS; PR00480; ASTACIN.
R PROSITE; PS00142; ZINQ_PROTEASE; 1.
R PROSITE; PS001010; ASX_HYDROXYL; 2.
R PROSITE; PS001010; ASX_HYDROXYL; 2.
R PROSITE; PS001010; ASX_HYDROXYL; 2.
R PROSITE; PS001187; EGF_2; 2.
R PROSITE; PS01187; EGF_2; 2.
R PROSITE; PS01187; EGF_2; 3.
R Metalloprotease; EGF_1ike domain; Zinc; Calcium; Signal; Glycoprotein; Zymogen; Alternative_splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NC (CATALYTIC) (BY SIMILARITY). SIMILARITY).
                                                                                                                           TISSUE SPECIFICITY: UBIQUITOUS.
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 5 CUB DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BONE MORPHOGENETIC PROTEIN METALLOPROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY
(BY
                                                               COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INC (CATALYTIC) (
INC (CATALYTIC) (
SIMILARITY.
SIMILARITY.
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                                                                                                                                                                                                                                                                             EMBL; U50330; AAA93462.1; -.
                                                                                                                                                                                                                                                                                        M22488; AAA51833.1; -. Y08723; CAA69973.1; -.
                                                                                                                                                                                                                                                                                                            EMBL; Y08724; CAA69974.1; EMBL; Y08725; CAA69975.1; EMBL; L35279; AAC41710.1; PIR; A37278; A37278. HSSP; P00736; 1APO.
                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000130; -.
InterPro; IPR000152; -.
InterPro; IPR000561; -.
InterPro; IPR000859; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
986
3321
434
434
5586
703
743
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859
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217
223
328
348
461
                                                                                                                     SPLICING
                                                                                                                                                                                                                                                                                                                                                                            MIM; 112264;
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DISULFID
DISULFID
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METAL
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                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                     EMBL;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
DKDESCKDUGGCOQDCVNTEGSYECQCR -> EKRPALOPP
RGRPHQLKPRYOKRNRTPO (IN ISOFORM BMP1-1).
MISSING (IN ISOFORM BMP1-1).
                                                                                                                                                                                                                                                                                                                                        IVPKYEVNGVKPPIGQR -> VLHSSLLLLSCGSRNGASFP
CSLESSTHQALCWTGLFLRPSPFPRLPLAAPRTLRAGV
                                                                                                                                                                                                                                                                                                                    QEY NFLKMEPQEVESLGETYDFDSIMHYARNTFSRGIFLDT
                                                                                                                                                                                                                                                                                                                                                                                                                   -> GCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fukagawa M., Noboru S., Hogan B.L.M., Jones C.M.;
"Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1),
which is related to the Drosophila dorsoventral gene tolloid and
encodes a putative astacin metalloendopeptidase.";
Dev. Biol. 163:175-183(1994).
-!- FUNCTION: CLEAVES THE C-TERMINAL PROPEPTIDES OF PROCOLLAGEN I, II
AND II. INDUCES CARTILAGE AND BONE FORMATION.
-!- CATALYTIC ACTIVITY: CLEAVAGE OF THE C-TERMINAL PROPEPTIDE AT
ALA-|-ASP IN TYPE I AND II PROCOLLAGENS AND AT ARG-|-ASP IN TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.19) (BMP-1)
(PROCOLLAGEN C-PROTEINASE) (PCP) (MAMMALIAN TOLLOID PROTEIN) (MTLD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKDECSKDNGGCQQD -> GGELFGLLGHPPRRP (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
ENZYME REGULATION: ACTIVITY IS INCREASED BY THE PROCOLLAGEN C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                 DLQVGKPLLWDRHCFRLSTHGPEMLGTALRG (IN
                                                                                                                                                                                                                                                                                                                                                                             (IN ISOFORM BMP1-4).
MISSING (IN ISOFORM BMP1-4).
AACGGFLTKLNGSITSPGWPKEYPPNKNCIWQLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISOFORM BMP1-5).
MISSING (IN ISOFORM BMP1-5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IN ISOFORM BMP1-6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111248 MW; F89201913AC3CBEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D -> N (IN REF. 4).
R -> S (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISOFORM BMP1-6)
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                                                                                           SIMILARITY. SIMILARITY.
                                                                                                                              SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. No. 8.1 ive 0; Mismatches
                                                      SIMILARITY
                                                                           SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.3%; Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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MEDLINE-94229342; PubMed-8174772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.3
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                              986
622
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 510
553
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572
772
772
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730
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717
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748
934
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P98063;
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991 AA; 111607 MW; 68A1847783A0BB9E CRC64;
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   SEQUENCE
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                                                                                                                      RESULT 10
MERK_MOUSE
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                                                   Matches
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                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
ENDOPEPTIDASE ENHANCER PROTEIN.
TISSUE SPECIFICITY: AT HIGH LEVELS IN EMBRYONIC MATERNAL DECIDUUM
AND FLOOR PLATE REGION OF THE NEURAL TUBE. LESS IN DEVELOPING
MEMBRANOUS AND ENDOCHONDRAL BONE, SUBMUCOSA OF INTESTINE, DERMIS
OF SKIN AND THE MESENCHYME OF SPLEEN AND LUNG.
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 5 CUB DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (2INC
METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CUB 3.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
CUB 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                               R InterPro; IPR000859; --
R InterPro; IPR000859; --
R InterPro; IPR001506; --
R InterPro; IPR001881; --
R Pfam; PF00431; CUB; 5.
R Pfam; PF00008; BGF; 2.
R Pfam; PF00008; BGF; 2.
R PRIMES; PR00048; ASTACIN.
R PROSITE; PS00142; ZINC_PROTBASE; 1.
R PROSITE; PS001180; CUB; 5.
R PROSITE; PS00120; ASTACIN.
R PROSITE; PS001180; CUB; 5.
R PROSITE; PS01186; EGF_1; FALSE_NEG.
R PROSITE; PS01186; EGF_2; 2.
R PROSITE; PS01186; EGF_2; 2.
R Growth factor; Cytokine; Repeat; Bone; Cartilage; Hydrolase; M Metalloprotease; EGF_1ike domain; Zinc; Calcium; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY) SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  BONE MORPHOGENETIC PROTEIN METALLOPROTEASE.
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(BY
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ZINC (CATALYTIC) (
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         402
466
515
515
577
577
622
671
                                                                                                                                                                                                                     InterPro; IPR000130; -
                                                                                                                                                                                                                                 InterPro; IPR000152; -
                                                                                                                                                                                                                                         InterPro; IPR000561; -
                                                                                                                                                                                                 MEROPS; M12.005; -. MGD; MGI:88176; Bmp1.
                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Zymogen
                                                                                                                                                                                          1APO.
                                                                                                                                                                                          P00736;
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METAL
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                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CD-1; TISSUE=Testis;
Dowds C.A., Burks D.J., Saling P.M.;
M. CDNA encoding part of a novel putative receptor tyrosine kinase.";
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q.
                                                                 Gaps
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-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

-!- TISSUE SPECIFICITY: SEEMS TO BE EXPRESSED PREDOMINANTLY IF NOT

EXCLUSIVELY IN THE MONOCYTIC LINEAGE.

-!- DEVELOPMENTAL STAGE: EXPRESSED DURING MOST, IF NOT ALL, STAGES OF

EMBRYOLOGICAL DEVELOPMENT BEGINNING IN THE MORULA AND BLASTOCYST

AND PROGRESSING THROUGH THE YOLK SAG AND FETAL LIVER STAGES.

-!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE MER PRECURSOR (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and developmental expression analysis of the murine c-mer tyrosine kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Graham D.K., Bowman G.W., Dawson T.L., Stanford W.L., Earp H.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AXL/UFO SUBFAMILY.
SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                 0;
Length 991;
                                                                 0; Indels
core 8; DB 1;
Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                                                                        994 AA
                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (RECEPTOR TYROSINE KINASE MERTK).
      Score 8;
                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-Spleen;
MEDLINE-95303502; PubMed-7784083;
                                                                 ;
                                                                                                                                                                                                                                                                                                                                                 MERK_MOUSE STANDARD; F 060805; 062194; 01-0cr-2000 (Rel. 40, Created) 01-0cr-2000 (Rel. 40, Last sequent-2000 (Rel. 40, Last sequent-2000 (Rel. 40, Last annotation)
   2.3%; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 472-994 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oncogene 10:2349-2359(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U21301; AAA80222.1; -. EMBL; L11625; AAA85355.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00069; pkinase; 1.
                                                                    8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR00177; -. InterPro; IPR003006; -. Pfam; PF00041; fn3; 2. Pfam; PF00047; ig; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:96965; Mer.
InterPro; IPR000719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MERTK OR MER.
Mus musculus (Mouse).
      Query Match
Best Local Similarity
                                                                                                                               104 CKYDFVEV 111
                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Snodgrass H.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
(BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTO-ONCOGENE TYROSINE-PROTEIN KINASE
                                                                         -i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY)
                   Hum. Mol. Genet. 9:645-651(2000).
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                            (POTENTIAL)
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PROSITE; PSO0107; PROTEIN_KINASE_ATP; 1.
PROSITE; PSO0109; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding; Transferase; Phosphorylation; Transmembrane; Signal; Repeat; Immunoglobulin domain; Proto-oncogene.

1 18 POTENTIAL.
                                                                                                                           -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES
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ATP (BY SIMILARITY)
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        dystrophic RCS rat.";
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Best Local Similarity
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ID DSG3_HUMAN
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                         PROTO-ONCOGENE TYROSINE-PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D'Cruz P.M., Yasumura D., Weir J., Matthes M.T., Abderrahim H.,
LaVail M.M., Vollrath D.;
"Mutation of the receptor tyrosine kinase gene Mertk in the retinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
PROTO-0COGENE TYROSINE-PROTEIN KINASE MER PRECURSOR (EC 2.7.1.112)
(C-MER) (RECEPTOR TYROSINE KINASE MERTK).
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PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00119; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DON; 1.
Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding; Transferase; Phosphorylation; Transmembrane; Signal; Repeat;
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I -> V (IN REF. 2).
603C09FAllF76FE0 CRC64;
                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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100.0%; Pred. No. 8.2;
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                                                                                    Immunoglobulin domain; Proto-oncogene
SIGNAL 1 18 POTENTIA
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MEDLINE=20164303; PubMed=10699188;
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CONFLICT
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STANDARD;

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RESULT 13 POLG\_HCVJ6

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                             DISEASE: PÉMPHIGUS VULGARIS (PV) IS A POTENTIALLY LETHAL SKIN
DISEASE IN WHICH EPIDERMAL BLISTERS OCCUR AS THE RESULT OF THE
LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY.
                                                                                                                                                                                                                                                       FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION.
         01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
DESMOGLEIN 3 PRECURSOR (130 KDA PEMPHIGUS VULGARIS ANTIGEN) (PVA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell adhesion; Signal; Transmembrane; Cytoskeleton; Glycoprotein; Calcium-binding; Repeat.
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                             MEDLINE=92069753; PubMed=1720352;
Amagai M., Klaus-Kovtun V., Stanley J.R.;
"Autoantibodies against a novel epithelial cadherin in pemphigus
                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL, ESOPHAGUS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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CADHERIN 4.
DESMOGLEIN REPEAT 1.
DESMOGLEIN REPEAT 2.
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CADHERIN 2.
                                                                                                                                                                                                                            vulgaris, a disease of cell adhesion.";
Cell 67:869-877(1991).
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N-LINKED
N-LINKED
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Pfam; PF00028; cadherin; 4.
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2568
383
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                                                                                       Homo sapiens (Human)
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MIM; 169615; -.
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999 AA;
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                                                                                                                                     NCBI_TaxID=9606;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-9204440; PubMed-1658196;
A Okamoto H., Okada S.-I., Sugiyama Y., Kurai K., Lizuka H.,
A Machida A., Miyakawa Y., Mayumi M.;
Machotida A., Miyakawa Y., Mayumi M.;
Machotida Sequence of the genomic RNA of hepatitis C virus isolated from a human carrier: comparison with reported isolates for conserved and divergent regions. ").

Gen. Virol. 72:2697-2704(1991).
L. J. Gen. Virol. 72:2697-2704(1991).
C -!- FUNCTION: THE SMALL PROFEINS NS2B, NS4A AND NS4B ARE
HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
C --- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPETIN M AND GLYCOPROTEIN E. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN C AND MRNA.
                         01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN) (P22);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polyprotein; Glycoprotein; Transferase; RNA-directed RNA polymerase; Core protein; Coat protein; Envelope protein; Helicase; ATP-binding; Transmembrane; Nonstructural protein; Hydrolase; Serine protease.
                                                                                                                                      ENVELOPE GILCOPROTEIN EL (GP32) (GP35); ENVELOPE GILCOPROTEIN (CP68) (GP69) (MS1); PROTEIN P7; NONSTRUCTURAL PROTEIN NS2 (P21) (EC 3.4.22.-); PROTEIN P7; NONSTRUCTURAL PROTEIN NS2 (P21) NONSTRUCTURAL PROTEIN NS4 (P4); NONSTRUCTURAL PROTEIN NS4B (P27); NONSTRUCTURAL PROTEIN NS5A (P56); NONSTRUCTURAL PROTEIN NS5B (P66) (P70) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48)].

Whenetitis C virus (isolate HC-16) (HCV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
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PP01538; HCV_NS2; 1.
PP01006; HCV_NS4a; 1.
PP01001; HCV_NS4b; 1.
PP01506; HCV_NS5a; 1.
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HCV_core; 1.
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InterPro; IPR002521;
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InterPro; IPR001490;
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MEROPS; S29.001; -.
MEROPS; U39.001; -.
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Pfam; PF01539;
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Query Match 2.3%; Sc Best Local Similarity 100.0%; P Matches 8; Conservative 0;

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TISSUE SPECIFICITY: EXPRESSED IN ONLY ONE CELL GROUP IN THE
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                             NONSTRUCTURAL PROTEIN NS4A (POTENTIAL)
NONSTRUCTURAL PROTEIN NS4B (POTENTIAL)
                                                                           NONSTRUCTURAL PROTEIN NS1 (POTENTIAL).
NONSTRUCTURAL PROTEIN NS2 (POTENTIAL).
PROTEASE/HELICASE NS3 (POTENTIAL).
REMOVED FROM CAPSID PROTEIN C BY THE
                             CAPSID PROTEIN C (POTENTIAL).
MATRIX PROTEIN (POTENTIAL).
MAJOR ENVELOPE PROTEIN E (POTENTIAL)
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01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
GONADOLIBERIN II PRECURSOR (GONADOTROPIN-RELEASING HORMONE II)
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CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
                  CELLULAR AMINOPEPTIDASE
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MEDLINE=94151343;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GONADOLIBERIN II.

GNRH-ASSOCIATED PEPTIDE II-1 (POTENTIAL)
GNRH-ASSOCIATED PEPTIDE II-2 (POTENTIAL)
PYRROLIDONE CARBOXYLIC ACID.
AMIDATION (G-34 PROVIDE AMIDE GROUP).
CF8COEDBF277365F CRC64;
                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002012; -...
Pfam; PF00446; GRRH; 1.
PROSITE; PS00473; GRRH; 1.
Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Elizur A., Zohar Y.,
"Levels of the native forms of GnRH in the pituitary of the gilthead
seabream, Sparus aurata, at several characteristic stages of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei; Sparidae; Sparus.
NCBI_TaxID=8175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
GONADOLIBERIN I PRECURSOR (GONADOTROPIN RELEASING HORMONE II)
(GNRH-II) (LH-RH II) (LULIBERIN II)
(SARH-II) (LH-RH II) (LOLIAGA sea bream)
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Powell J.F.F., Zohar Y., Elizur A., Park M., Fischer W.H., Craig A.G., Rivier J.E., Lovejoy D.A., Sherwood N.M.; "Three forms of gonadotropin-releasing hormone characterized from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Proc. Natl. Acad. Sci. U.S.A. 91:12081-12085(1994).

-i- FUNCTION: STIMULAR THE SECRETION OF GONADOTROPINS.

-i- MASS SPECTROMERRY: MW=1236.6; METHOD=MALDI; RANGE=24-33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROGONADOLIBERIN II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
. 9.8;
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Pred. No. 9.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 AA.
-! - SIMILARITY: BELONGS TO THE GNRH FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gen. Comp. Endocrinol. 112:394-405(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.0%; Sco.
100.0%; Pre
0;
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MEDLINE=99061849; PubMed=9843645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95083645; PubMed=7991588;
                                                                                                                                                                                                                                                                                                              EMBL; L27435; AAA74993.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal; Multigene family. SIGNAL 1 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                              EMBL; U30325; AAA7547.1; -.
InterPro; IPR002012; -.
Pfam; PF00446; GnRH; 1.
PROSITE; PS004473; GNRH; 1.
Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus; Signal.
1 23
CHAIN 24 85 PROGONADOLIBERIN II.
                                                                                                                                                                                                                                                                                               GONDADOLIBERIN II.
GURH-ASSOCIATED PEPTIDE II.
PYRROLIDONE CARBOXYLIC ACID.
AMIDATION (G-34 PROVIDE AMIDE GROUP).
B53165C1227722CC CRC64;
SIMILARITY: BELONGS TO THE GNRH FAMILY.
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85
33
85
24
33
9543 MW;
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MOD_RES
SEQUENCE
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PEPTIDE
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Search completed: September 5, 2001, 10:58:05 Job time: 117 sec

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Gaps

; 0

Length 85; 0; Indels

Query Match 2.0%; Score 7; DB 1; Best Local Similarity 100.0%; Pred. No. 9.8; Matches 7; Conservative 0; Mismatches

2 LLLGLLL 8 ||||||| 8 LLLGLLL 14

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364 14 Q68816 371 4 Q16748 371 4 Q16746 495 4 Q16742 495 4 Q16742	495 4 3018 14 3019 14 3019 14	31 11 Q9QVA5 33 11 Q9QVJ4 41 11 Q9QUY1 86 4 Q9HZW9	94 4 Q9HZW8 116 10 P93284 221 2 Q9KU56		347 8 Q9MG10 350 4 Q9MG10	364 14 364 14 364 14	364 14 Q68814	ALTGNMENTS		13, Created) 13, Last sequence 16, Last annotati	use). oa; Chordata; Craniata; Vertebrata; Euteleostomi; ia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. ;		C TISSUE=OVARY; A Tsai YJ., Lee R.KK., Chen YH., Lin SP., Cheng W.TK.; I "CDMA cloning of fallotein from mouse ovary."; C.hmittad (INV.100) to the ENDY Company (INDI Astheory)	9.9.5 Lo the Embally Cell Bally Green accessors. 84822516.1; 072;	859; UB; 1. Cmp 1.	. PDGF_1. CUB: 0.1	A; 50/41 MW; 5AJOALF/ULDG4EA& CRCG4;	100.0%; Score 345; DB 11; Length 345; .larity 100.0%; Pred. No. 0; .Conservative 0; Mismatches 0; Indels 0; Gaps 0;	MLLIGLLLLTSALAGORTGTRAESNLSSKLÖLSSDKEQNGVQDPRHERVVTISGNGSIHS 60 	PKFPHTYPRNWVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL 120 	GRWCGSGTVPGKOTSKGNHIRIRFVSDEVFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS 180
20 20 22 22 23 23 23 24 24 25 26 26 27 26 27 27 27 27 27 27 27 27 27 27 27 27 27	Seconds 26 9 2 27 9 2 28 9 2 2 29 9 2 2 2 2 9 2 2 2 2 9 2 2 2 2	31 8 2 3 3 8 2 3 3 4 5 3 3 3 8 8 2 3 3 4 5	w w w	0 00 00 0 00 00	ο & α	0 00 00 0	0 00		SULT 1 2Y71 090Y71	Q9QY71; 01-MAY-2000 01-MAY-2000 01-MAR-2001	DE FALLOTEIN. OS Mus musculus (Mouse). OC Eukaryota; Metazoa; Chordata, OC Mammalia; Eutheria; Rodentia, OX NCBI TaxID=10090;	E. E.	a Racinted, R	DR InterPro; IPR0000	DR InterPro; IPR0008 Description DR Pfam; PF00431; CU	mus musculu D	ā	gallus gall Query Match omo sapien Best Local Simi hepatitis c Matches 345;	Qy 1	hepatitis c Qy 61 hepatitis c Db 61 hepatitis c Db 61	hepatitis c Apatitis c Apatitis c Apatitis c
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	September 5, 2001, 10:55:48 ; Search time 24 (without alignme 1845.743 Million	Title: US-09-457-066-43 Perfect score: 345 Sequence: 1 MLLIGLLLISALAGORTGTDVALEHHEECDCVCRGNAGG	Scoring table: OLIGO Gapop 60.0 , Gapext 60.0	Searched: 425026 seqs, 132305027 residues	Word size : 0	er of hits sa	0000000	Post-processing: Listing first 45 summaries	Database : SPTREMBL_16:* 1: sp_archea:* 2: sp_bacteria:* 3: sp_fungi:* 4: sp_human:*		9: sp_phage:* 10: sp_plant:* 11: sp_rodent:* 12: sp_unclassified:* 13: sp_vertebrate:*	14: sp_virus:*	Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being puand is derived by analysis of the total score distribution.	SUMMARIES	Result Query No. Score Match Length DB ID	345 100.0 345 11 Q9QY71 102 29.6 345 11 Q9JHV8	73 42.19 345 4 Q9URA 52 15.1 345 4 Q9URA 52 15.1 345 4 Q9NRA1	32 9.3 345 13 091946 9 2.6 97 4 016755 9 2.6 364 14 068809	9 9 2.6 364 14 Q96851 0 9 2.6 364 14 Q96851 1 9 2.6 364 14 Q96855 2 9 2.6 364 14 Q96855	3 9 2.6 364 14 Q96858 4 9 2.6 364 14 P87755 5 9 2.6 364 14 Q68789 6 9 2.6 364 14 Q68795	9 2.6 364 14 Q68800 9 2.6 364 14 Q68803 9 2.6 364 14 Q68812

TISSUE=KIDNEY;

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STRAIN-WISTAR;
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                                                                    SEQUENCE
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GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS 180
                                                                241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300
                                                                              SEQUENCE FROM N.A. STRAIN=SWISS-WEBSTER/NIH; STRAIN=SWISS-WEBSTER/NIH; Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.; "The mouse Pdgfc gene: Dynamic expression in embryonic tissues during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 TVPGKQISKGNHIRIRIREVSDEYFPSEPGFCIHYSIIMPQVIETITSPSVLPPSSLSLDLLN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 TVPGKQTSKGNHIRIREVSDEYFPSEPGFCIHYSLIMPQVTETTSPSVLPPSSLSLDLLN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                   LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                              VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
                                                                                                                          301 VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FA1486BED6D362F8 CRC64;
                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PLATELET-DERIVED GROWTH FACTOR C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 NAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLY 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 NAVTAFSTLEELIRYLEPDRWQVDLDSLYRPTWQLLGKAFLY 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 102; DB 11;
Pred. No. 2.9e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.6%; Scor. 100.0%; Pred. No. 2... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , CUB; 1.
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PROSITE; PS50278; PDGF_2; 1.
SMART; SM00042; CUB; 1.
SEQUENCE 345 AA; 38886 MW
                                                                                                                                                                                                                                                                                                                                                                                      Mech. Dev. 0:0-0(2000).
EMBL; AF286725; AAF91483.1;
InterPro; IPR000072; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000859; -.
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Best Local Similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00431; CUB;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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                      181
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Q9JHV8
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099E0X6
IID 099
ID 090
DT 011
DT 011
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                                                                                                                                                                                                                                                                                            236 VNLNLLKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQ 295
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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01-MAR-2001 (TTEMBLFE]. 16, Last annotation update)
SECRETORY GROWTH FACTOR-LIKE PROTEIN FALLOTEIN (SPINAL CORD-DERIVED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Hamada T., Ui-Tel K., Imaki J., Miyata Y.;
"Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous SCDGF-DGF-C/fallotein.";
Bloochem. Bloophys. Res. Commun. 0:0-0(2000).
EMBL; AB033830; BAB19969.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUB=UTBRUS;
Tsai Y.J., Lee R.K.K., Lin S.P.;
"Fallotein, a novel growth factor like gene identified in human
                                                                                                                                                                                                                                              ;
0
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                                                                                                                                                                                           Score 79; DB 11; Length 345;
Pred. No. 8.6e-69;
0; Mismatches 0; Indels
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2.1e-42;
thes 0; Indels
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                                                                                                             830; BABIYYOY.1; -.
345 AA; 38734 MW; F296DA6E9B765D10 CRC64;
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Pred. No. 2.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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100.0%; Pre-
0; }
                                                                                                                                                                     22.9%; Scc.
100.0%; Pre
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SEQUENCE 345 AA; 39029 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                 296 CVPRKVTKKYHEVLQLRPK 314
                                                                                                                                                                                                                                                                                                                                                                                        296 CVPRKVTKKYHEVLQLRPK 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 13, TrEMBLrel. 13, (TrEMBLrel. 16,
                                                                                                                                                                                             Query Match 22.9°
Best Local Similarity 100.
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 15.13
Best Local Similarity 100.0
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000072; -.
InterPro; IPR000859; -.
Pfam; PF00341; PDGF; 1.
Pfam; PF00431; CUB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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Gaps

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Indels

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Q9NRA1

Q9NRA1

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SEQUENCE FROM N.A.
TISSUE-PERIPHERAL BLOOD;
MEDLINE-93024490; PubMed-1406709;
Helmberg A., Tusie-Luna M.T., Tabarelli M., Kofler R., White P.C.;
"R339H and P4538: CYP21 mutations associated with nonclassic steroid
21-hydroxylase deficiency that are not apparent gene conversions.";
Mol. Endocrinol. 6:1318-1322(1992).
-!- CATALYTIC ACTIVITY: A STEROID + AH(2) + O(2) = A 21-HYDROXYSTEROID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tokita H., Okamoto H., Iizuka H., Kishimoto J., Tsuda F., Lesmana L.A., Miyakawa Y., Mayumi M.; "Hepatitis C virus variants from Jakarta, Indonesia classifiable into novel genotypes in the second (2e and 2f), tenth (10a) and eleventh (11a) genetic groups."; J. Gen. Virol. 77:293-301(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
U-MAR-2001 (TrEMBLrel. 16, Last annotation update)
STEROID 21-MONOXYGENASE (EC 1.14.99.10) (STEROID 21-HYDROXYLASE)
(CYTOCHROME P450 XXIA1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL; X58908; CAA41711.1; -.
Interpro; IPRO01128; -.
Pfam; PF00067; P450; 1.
Heme; Monooxygenase; Oxidoreductase.
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
        Pred. No. 7.4e-23;
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100.0%; Pred. No. 0.78;
ive 0; Mismatches
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                               Mismatches
                                                                  IQLTFDERFGLEDPEDDICKYDFVEVEEPSDG 117
                                                                                    97
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last anno
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MEDLINE=96226020; PubMed=8627233;
100.0%; Pro
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-!- COFACTOR: HEME-THIOLATE.
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Best Local Similarity 100.
Matches 9; Conservative
                               Conservative
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                                                                                                                                                                                                            PRELIMINARY;
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      Best Local Similarity
Matches 32; Conserv
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SEQUENCE
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Q16755
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Q68809
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MEDLINE=20317014; PubMed=10858496;
Hamada T., U1-Tei K., Miyata Y.;
"A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VEGF family.";
FEBS Lett. 475:97-102(2000).
EMBL; AB033829; BAB03265.1; -.
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                  Li X., Ponten A., Aase K., Karlsson L., Abramsson A., Uutela M.,
Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P.,
Betsholtz C., Heldin C.-H., Alitalo K., Ostman A., Eriksson U.;
"PDGF-C is a novel protease-activated ligand for the PDGF alpha
I receptor.";
IN Nat. Cell Biol. 00-0(2000).
R EMBL; AF244813; AAF80597.1; -.
R InterPro; IPR000072; -.
R InterPro; IPR000859; -.
R Fam. PPG0431; CUB; 1.
R PROSITE; PS01180; CUB; 1.
R PROSITE; PS01180; CUB; 1.
R PROSITE; PS01180; CUB; 1.
                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
SPINAL CORD-DERIVED GROWTH FACTOR.
GADGE.
Gallus gallus (Chicken).
                                             Q9NRA1;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 16, Last annotation update)
PLATELET-DERIVED GROWTH FACTOR C.
HOMO sapiens (Human).
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PROSITE; PS50278; PDGF_2; 1.
SMART; SM00042; CUB; 1.
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SEQUENCE 345 AA; 3
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InterPro; IPR000859;
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Q91946 Q91946;

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RESULT Q91946

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Indels Length 97;

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Lizuka H., Mishiro S., Miyakawa Y., Mayumi M.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A.
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SEQUENCE
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1. GENEL: SIMILARITY: TO HEPATITIS C. VIRUS RNA DEPENDENT RNA POLYMERASE.

EMBL: D37855; BAA07098.1;
                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Hepacivirus.
EMBL; D49768; BAA08602.1; -.
InterPro; IPR002166; -.
Pfam; PF00998; HCV_RGRP; 1.
Nonstructural protein; Polyprotein; RNA-directed RNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR002166; -...
Pfam; PF00998; HCV_RdRP; 1.
Nonstructural protein; Polyprotein; RNA-directed RNA polymerase.
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                                                                                                                                                            2.6%; Score 9; DB 14; Length 364;
100.0%; Pred. No. 2.3;
ive 0; Mismatches 0; Indels
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                                                                                                   74BF8B2BD95964D3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                               081599;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GENOME POLYPROTEIN (FRAGMENT).
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100.0%; Pred. No. ...
0; Mismatches
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01-FEB-1997 (TrEMBLrel. 02, Last sequ
01-MAR-2001 (TrEMBLrel. 16, Last ann
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                                                                                                   364 AA; 40181 MW;
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Best Local Similarity 100..
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Best Local Similarity
The 9; Conserv?
                                                                                                                                                                                                                                                                 345 LLEGLELLT 353
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NCBI_TaxID=11103;
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SEQUENCE
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081599
AC 081599
AC 081599
DT 01-NOV.
DT 01-NOV.
DT 01-NAP.
DE GENOME
OC VITUSEE
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STRAIN-VN506;
MEDLINE-9506197; PubMed-7972001;
Tokita H., Okamoto H., Tsuda F., Song P., Nakata S., Chosa T.,
Tokita H., Mishiro S., Miyakawa Y., Mayumi M.;
"Hepatitis C virus variants from Vietnam are classifiable into the
seventh, eighth, and ninth major genetic groups.";
Proc. Natl. Acad. Sci. U.S.A. 91:11022-11026(1994).
EMBL; D87356; BAA13399.1; -.
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Hepacivirus
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STRAIN-VESS.

MEDLINE=95062197; PubMed=7972001;

MEDLINE=95062197; PubMed=7972001;

Tokita H., Okamoto H., Tsuka F., Song P., Nakata S., Chosa T.,

Tizuka H., Mishiro S., Miyakawa Y., Mayumi M.;

"Hepatitis C virus variants from Vietnam are classifiable into the seventh, and ninth major genetic groups.";

Proc. Natl. Acad. Sci. U.S.A. 91:11022-11026(1994).

-1- SIMILARITY: TO HEPATITIS C VIRUS RNA DEPENDENT RNA POLYMERASE. InterPro: IPR00166;

-1- FIGHT PROSIGES.

PFO0999; HCV_RGRP? 1.
                                                                                                                                                                                                                                              Interpro; IPR002166; -.
Pfam; PF00998; HCV_RGRP; 1.
Nonstructural protein; Polyprotein; RNA-directed RNA polymerase.
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Submitted (AUG-1996) to the EMBL/GenBank/DDbJ databases.
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-!- SIMILARITY: TO HEPATITIS C VIRUS RNA DEPENDENT RNA POLYMERASE
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Iizuka H., Mishiro S., Miyakawa Y., Mayumi M.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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Iizuka H., Mishiro S., Miyakawa Y., Mayumi M.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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100.0%; Pred. No. 2.3;
tive 0; Mismatches 0; Indels
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GENOME POLYPROTEIN (FRAGMENT).
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345 LLLGLLLT 353
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Tokita H., Okamoto H., Tizuka H., Kishimoto J., Tsuda F.,
Lesmana L.A., Miyakawa Y., Mayumi M.;
"Hepatitis C virus variants from Jakarta, Indonesia classifiable into novel genotypes in the second (2e and 2f), tenth (10a) and eleventh (11a) genetic groups.";
J. Gen. Virol. 77:293-301(1996).
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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InterPro; IPR002166; -.
Pfam; PF00998; HCV_RGRP; 1.
Nonstructural protein; Polyprotein; RNA-directed RNA polymerase.
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Pfam; PF00998; HCV_RdRP; 1.
Nonstructural protein; Polyprotein; RNA-directed RNA polymerase.
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100.0%; Pred. No. 2.3;
ive 0; Mismatches 0; Indels
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GENOME POLYPROTEIN (FRAGMENT).
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MEDLINE=96226020; PubMed=8627233;
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01-NOY-1996 (TrEMBLEE) 01, La
01-MAR-2001 (TrEMBLEE): 16, La
GENOME POLYPROTEIN (FRAGMENT).
EMBL; D87363; BAA13346.1;
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MEDLINE-96226020; PubMed-8627233;
Tokita H., Okamoto H., Iizuka H., Kishimoto J., Tsuda F.,
Tokita H., Okamoto H., Iizuka H., Kishimoto J., Tsuda F.,
Lesmana L.a., Miyakawa Y., Mayumi M.;
Tesmana L.a., Miyakawa Y., Mayumi M.;
The over a construction of the second (2e and 2f), tenth (10a) and eleventh of the second (2e and 2f), tenth (10a) and eleventh of the genetic groups.";
Token Virol. 77:293-30(1996).
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